

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
SEQUENCE LISTING

<110> Genentech, Inc.  
Ashkenazi, Avi  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Filvaroff, Ellen  
Fong, Sherman  
Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, A.  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth, J.  
Kljavin, Ivar J.  
Mather, Jennie P.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William, I.

<120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

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His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
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Page 3

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290

295

300

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&lt;212&gt; DNA

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&lt;211&gt; 379

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens



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Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile  
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Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln  
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Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys  
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195 200 205  
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys  
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Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn  
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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 11

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys  
 35 40 45  
 Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu  
 50 55 60  
 Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
 65 70 75 80  
 Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
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 Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
 100 105 110  
 Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
 115 120 125  
 Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln  
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 oligonucleotide probe

<400> 16  
 ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg 50

<210> 17  
 <211> 960  
 <212> DNA  
 <213> Homo sapiens

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;400&gt; 17

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gctgcttgcc ctgttgatgg caggcttggc cctgcagcca ggcactgccc tgctgtgcta 60
ctcctgcaaa gcccagggtga gcaacgagga ctgcctgcag gtggagaact gcacccagct 120
gggggagcag tgctggaccg cgcgcattccg cgcagttggc ctctgaccg tcatcagcaa 180
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cacgtgctgt gacaccgact tgtgcaacgc cagcggggcc catgccctgc agccggctgc 300
cgccatcctt gcgctgctcc ctgcactcgg cctgctgctc tggggaccg gccagctata 360
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tcctcacaga cctggcccag tgggagcctg tcctggttcc tgaggcacat cctaacgcaa 480
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ggactcccac ccggcagatc agctctagtg acacagatcc gcctgcagat ggccccctcca 600
accctctctg ctgctgtttc catggcccag cattctccac ccttaaccct gtgctcaggc 660
acctcttccc ccaggaagcc ttccctgccc accccatcta tgacttgagc caggtctggg 720
ccgtggtgtc ccccgacccc agcaggggac aggcactcag gagggcccag taaaggctga 780
gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagttcct gggagtctcc 840
agagatgggg cctggaggcc tggaggaagg ggccaggcct cacattcgtg gggctcccgt 900
aatggcagcc tgagcacagc gtaggccctt aataaacacc tgttgataa gccaaaaaa 960

```

&lt;210&gt; 18

&lt;211&gt; 189

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

```

Met Thr His Arg Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val
 1          5          10          15
Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
          20          25          30
Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
 35          40          45
Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50          55          60
Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65          70          75          80
Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
          85          90          95
Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
100          105          110
Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
115          120          125
Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
130          135          140
Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
145          150          155          160
Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
165          170          175
Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
180          185

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&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 19

tgctgtgcta ctcctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 20

tgcaacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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gaccgaccag	ctgagcaggc	ggcagatccg	cgagtaccaa	ctctacagca	ggaccagtgg	180
caagcacgtg	caggtcaccg	ggcgtcgcgt	ctccgccacc	gccgaggacg	gcaacaagtt	240
tgccaagctc	atagtggaga	cggacacggt	tggcagcccg	gttcgcatca	aaggggctga	300
gagtggagaag	tacatctgta	tgaacaagag	gggcaagctc	atcgggaagc	ccagcgggaa	360
gagcaaaagac	tgcgtgttca	cggagatcgt	gctggagaac	aactatacgg	ccttccagaa	420
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acgaccaggg	cctgcacccc	accccccaact	cccagccccc	gaataaaacc	attttcctgc	1200

<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23

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Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
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Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
          20          25          30
Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
          35          40          45
Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
          50          55          60
Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
          65          70          75          80
Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
          85          90          95
Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
          100          105          110
Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
          115          120          125
Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
          130          135          140
Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
          145          150          155          160
Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
          165          170          175
His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
          180          185          190
Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
          195          200          205

```

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 24

cagtacgtga gggaccaggg cgccatga

28

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe



## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;400&gt; 25

ccggtgacct gcacgtgctt gcca

24

&lt;210&gt; 26

&lt;211&gt; 41

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (21)..(21)

&lt;223&gt; a, t, c or g

&lt;400&gt; 26

gcggatctgc cgctgtctca nctggtcggg catggcgccc t

41

&lt;210&gt; 27

&lt;211&gt; 2479

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 27

acttgccatc	acctgttgcc	agtgtggaaa	aattctccct	gttgaatttt	ttgcacatgg	60
aggacagcag	caaagagggc	aacacaggct	gataagacca	gagacagcag	ggagattatt	120
ttaccatacg	ccctcaggac	gttccctcta	gctggagttc	tggacttcaa	cagaacccca	180
tccagtcatt	ttgattttgc	tgtttatttt	ttttttcttt	ttctttttcc	caccacattg	240
tattttatatt	ccgtacttca	gaaatgggccc	tacagaccac	aaagtggccc	agccatgggg	300
cttttttctt	gaagtcttgg	cttatcattt	ccctggggct	ctactcacag	gtgtccaaac	360
tcctggcctg	ccctagtgtg	tgccgctgcg	acaggaactt	tgtctactgt	aatgagcgaa	420
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ataacgatca	actccttaaa	ggagatttca	gactgcagcc	catttacacc	ccaaatgggg	2160
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tgggatttaa aaaaagtgtc atcttttcta tttcaagtta attacaaaca gttttgtaac 2460  
tccttgcttt ttaaattctt 2479

&lt;210&gt; 28

&lt;211&gt; 660

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu  
1 5 10 15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys  
20 25 30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
130 135 140

Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
145 150 155 160

Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
165 170 175

Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
180 185 190

Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
195 200 205

Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
210 215 220

Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
225 230 235 240

Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
245 250 255

Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
260 265 270

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
275 280 285

Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
290 295 300

Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
305 310 315 320

Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
325 330 335

Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
340 345 350

Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
355 360 365

Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
370 375 380

Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
385 390 395 400

Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg  
405 410 415

Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val  
420 425 430

Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met  
435 440 445

Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly  
450 455 460

Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu  
465 470 475 480

Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu  
485 490 495

Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala  
500 505 510

Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser  
515 520 525

His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala  
530 535 540

Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser  
545 550 555 560

Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys  
565 570 575

Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly  
580 585 590

Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln  
595 600 605

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu  
610 615 620

Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His  
625 630 635 640

Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu  
645 650 655

His Cys His Thr  
660

<210> 29  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29  
cggtctacct gtatggcaac c 21

<210> 30  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30  
gcaggacaac cagataaacc ac 22

<210> 31  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31  
acgcagattt gagaaggctg tc 22

<210> 32  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32  
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<210> 33  
<211> 3449  
<212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

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&lt;210&gt; 34

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 915

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

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Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
          20          25          30
Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
          35          40          45
Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
 50          55          60
Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
 65          70          75          80
Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
          85          90          95
Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
          100          105          110
Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
          115          120          125
His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
          130          135          140
Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
          145          150          155          160
Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
          165          170          175
Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
          180          185          190
Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
          195          200          205
Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
          210          215          220
Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His
          225          230          235          240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile
          245          250          255
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser
          260          265          270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His
          275          280          285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln
          290          295          300
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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325 330 335  
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu  
340 345 350  
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn  
355 360 365  
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr  
370 375 380  
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys  
385 390 395 400  
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu  
405 410 415  
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe  
420 425 430  
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu  
435 440 445  
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser  
450 455 460  
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys  
465 470 475 480  
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu  
485 490 495  
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu  
500 505 510  
Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
515 520 525  
Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
530 535 540  
Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
545 550 555 560  
Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
565 570 575  
Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
580 585 590  
Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
595 600 605  
Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
610 615 620  
Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
625 630 635 640  
Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
660 665 670  
Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
675 680 685  
Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
690 695 700  
Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
705 710 715 720  
Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
725 730 735  
Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
740 745 750  
Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
755 760 765  
Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
770 775 780  
Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
785 790 795 800  
Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
805 810 815  
Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
820 825 830  
Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
835 840 845  
Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
850 855 860  
Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
865 870 875 880  
Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
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<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 35



<210> 36  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 36  
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<210> 37  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 37  
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<210> 38  
 <211> 1813  
 <212> DNA  
 <213> Homo sapiens

<400> 38  
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 gggccatgat ttccctcccg gggcccctgg tgaccaactt gctgcggttt ttgttcctgg 180  
 ggctgagtgc cctcgcgccc ccctcgcggg ccagctgca actgcacttg cccgccaacc 240  
 ggttgagggc ggtggagggg ggggaagtgg tgcttcagc gtggtacacc ttgcacgggg 300  
 aggtgtcttc atcccagcca tgggaggtgc cctttgtgat gtggttcttc aaacagaaaag 360  
 aaaaggagga tcaggtgttg tcctacatca atgggggtcac aacaagcaaa cctggagtat 420  
 ccttggtcta ctccatgccc tcccgaacc tgccctcgc gctggagggt ctccaggaga 480  
 aagactctgg cccctacagc tgctccgtga atgtgcaaga caaacaaggc aaatctaggg 540  
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 tttgtatgaa aaa 1813

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;210&gt; 39

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

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Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu
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Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln
          20           25           30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
          35           40           45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
          50           55           60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
          65           70           75           80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro
          85           90           95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg
          100          105          110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val
          115          120          125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
          130          135          140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
          145          150          155          160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
          165          170          175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
          180          185          190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
          195          200          205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
          210          215          220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
          225          230          235          240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
          245          250          255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
          260          265          270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
          275          280          285
Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
          290          295          300

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
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 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335  
 Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350  
 Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365  
 Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380  
 Gln Ala Gly Ser Leu Val  
 385 390

<210> 40  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40  
 agggctctcca ggagaaagac tc 22

<210> 41  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41  
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<210> 42  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 42  
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<210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 43  
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<210> 44  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 44  
gaccggcagg cttctgcg 18

<210> 45  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 45  
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<210> 46  
<211> 24  
<212> DNA  
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<220>  
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oligonucleotide probe

<400> 46  
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<210> 47  
<211> 45  
<212> DNA  
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<220>  
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oligonucleotide probe

<400> 47  
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<210> 48  
<211> 2822  
<212> DNA  
<213> Homo sapiens

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tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240  
ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480
atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540
taggttacaa gaacaacact atctcagcca aggacaccct ttctaactca actcttactg 600
aatttgtaaa aaccgtgaat aattttgttc aaagggatac atttgtagtt tgggacaagt 660
tatctgtgaa tcataggaga acacatctta caaaactcat gcacactgtt gaacaagcta 720
ctttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780
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<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys  
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Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys  
20 25 30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe  
35 40 45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn  
50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly  
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn  
                                  100                                   105                                   110  
 Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys  
                                  115                                   120                                   125  
 Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln  
                                  130                                   135                                   140  
 Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile  
                                  145                                   150                                   155                                   160  
 Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys  
    165                                   170                                   175  
 Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr  
    180                                   185                                   190  
 Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val  
    195                                   200                                   205  
 Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys  
    210                                   215                                   220  
 Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe  
    225                                   230                                   235                                   240  
 Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys  
    245                                   250                                   255  
 Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met  
    260                                   265                                   270  
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    275                                   280                                   285  
 Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser  
    290                                   295                                   300  
 Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln  
    305                                   310                                   315                                   320  
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    325                                   330                                   335  
 Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys  
    340                                   345                                   350  
 Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser  
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 Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp  
    370                                   375                                   380  
 Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser  
    385                                   390                                   395                                   400  
 Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
405 410 415

Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln  
420 425 430  
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr  
435 440 445  
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys  
450 455 460  
Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
465 470 475 480  
Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
485 490 495  
Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
500 505 510  
Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe  
515 520 525  
Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
530 535 540  
Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
545 550 555 560  
Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
565 570 575  
Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
580 585 590  
Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
595 600 605  
Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
610 615 620  
Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
625 630 635 640  
Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
645 650 655  
Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
660 665 670  
Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
675 680 685  
Leu Arg  
690

<210> 50  
<211> 589  
<212> DNA  
<213> Homo sapiens  
<220>  
<221> modified\_base

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<222> (61)..(61)

<223> a, t, c or g

<400> 50

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ngaaaagccg	gcatatggat	tcaaatggca	atgttgcagt	tgcattttta	tattataaga	120
gtattggtcc	ctttgccttc	atcatctgac	aacttcttat	tgaaacctca	aaattatgat	180
aattctgaag	aggaggaaag	agtcatatct	tcagtaattt	cagtctcaat	gagctcaaac	240
ccaccacat	tatatgaact	tgaaaaaata	acatttacat	taagtcacg	aaaggtcaca	300
gataggata	ggagtctatg	tggcattttg	gaatactcac	ctgataccat	gaatggcagc	360
tggtcttcag	agggctgtga	gctgacatac	tcaaatagaga	cccacacctc	atgccgctgt	420
aatcacctga	cacattttgc	aattttgatg	tcctctggtc	cttcatttgg	tattaaagat	480
tataatattc	ttacaaggat	cactcaacta	ggaataatta	tttactgat	ttgtcttgcc	540
atatgcattt	ttaccttctg	gttcttcagt	gaaattcaaa	gcaccagga		589

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18



## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;210&gt; 55

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 55

ggatctcctg agctcagg

18

&lt;210&gt; 56

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 56

cctagttgag tgatccttgt aag

23

&lt;210&gt; 57

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

&lt;210&gt; 58

&lt;211&gt; 2137

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 58

```

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60
cgctaagcga ggcctcctcc tcccgcagat ccgaacggcc tgggcggggt caccctggct 120
gggacaagaa gccgccgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180
aggcgggggtg tgagtgggtg tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa 240
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cggcccggag ccgccgcgcc gtcagagcag gagcgtgcg tccaggatct agggccacga 360
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accccatcgc ccggagctgc gccgagagcc ccaggagggt gccatgcgga gcgggtgtgt 480
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cttctcggac gcggggcccc acgtgacta cggctggggc gaccccatcc gcctgcggca 600
cctgtacacc tccggcccc acgggctctc cagctgcttc ctgcgcaccc gtgccgacgg 660
cgctcgtggac tgcgcgcggg gccagagcgc gcacagtttg ctggagatca aggcagtcgc 720
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gctgcactgt ctgagttctg ctggaatacc tccatcgatg ggggaactcac ttcctttgga 1440
aaaattctta tgtcaagctg aaatttctta atttttctc atcacttccc caggagcagc 1500
cagaagacag gcagtagttt taatttcagg aacagggtgat ccactctgta aaacagcagg 1560
taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620
cccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680
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ggccagttct gtcatggatg ctgtcctgag aataacttgc tgtcccgtg tcacctgctt 1800
ccatctccca gccaccagc cctctgccca cctcacatgc ctccccatgg attggggcct 1860
cccaggcccc ccaccttatg tcaacctgca cttcttgttc aaaaatcagg aaaagaaaag 1920
atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagacctt 1980
gaaccctttc cccagcactt ggttttccaa catgatattt atgagtaatt tattttgata 2040
tgtacatctc ttattttctt acattattta tgccccaaa ttatatttat gtatgtaagt 2100
gaggtttggt ttgtatatta aaatggagtt tgtttgt 2137

```

&lt;210&gt; 59

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

```

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
 1          5          10          15
Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
          20          25          30
His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
          35          40          45
Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
          50          55          60
Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
          65          70          75          80
Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
          85          90          95
Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
          100          105          110
Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
          115          120          125
Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
          130          135          140
Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
          145          150          155          160
Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
          165          170          175
Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
          180          185          190
Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
          195          200          205
Val Arg Ser Pro Ser Phe Glu Lys
          210          215

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 60  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 60  
 atccgcccag atggctacaa tgtgta 26

<210> 61  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 61  
 gcctcccggg ctcctgagc agtgccaaac agcggcagtg ta 42

<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtccggg gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
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 gctgctgctg cgctacctgg tggcgcacct gggctatcat aaggcctatg ggttttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctatgt tagcctgcaa 240  
 aaccccaaag aagactgttt cctccagatt agagtggaaag aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360  
 tttcaatatc cggatcaaaa atgtgacaag aagtgatgag gggaaatatc gttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaaagtatt 480  
 agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggt 540  
 agagctacga tgtcaagaca aagaagggaa tccagctcct gaatacacat ggtttaagga 600  
 tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660  
 aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg aactggaga 720  
 atattcctgt gaagcccgcg attctgttgg atatcgagg tgccttgga aacgaatgca 780  
 agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840  
 ttccgtttgt ggcttgggtg tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900  
 ctcccttcag aagagtaatt cttcatctaa agccacgaca atgagtgaag atgtgcagtg 960  
 gctcacgcct gtaatcccag cactttggaa ggccgcggcg ggcggatcac gaggtcagga 1020  
 gttctagacc agtctggcca atatggtgaa accccatctc tactaaaata caaaaattag 1080  
 ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
 acccgggagg cggagggtgc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact gggtttttacc 1260  
tgtagaattc ttacaataaaa tatagcttga tattc 1295

<210> 64  
<211> 312  
<212> PRT  
<213> Homo sapiens

<400> 64  
Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
1 5 10 15  
Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
20 25 30  
Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
35 40 45  
Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
50 55 60  
Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
65 70 75 80  
Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
85 90 95  
Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
100 105 110  
Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
115 120 125  
Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
130 135 140  
Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
145 150 155 160  
Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
165 170 175  
Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
180 185 190  
Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
195 200 205  
Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
210 215 220  
Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
225 230 235 240  
Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
245 250 255  
Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
260 265 270  
Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
290 295 300

Gly Gly Ser Arg Gly Gln Glu Phe  
305 310

<210> 65  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 65  
atcgttgatga agtttagtgcc cc 22

<210> 66  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 66  
acctgcgata tccaacagaa ttg 23

<210> 67  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 67  
ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

<210> 68  
<211> 2639  
<212> DNA  
<213> Homo sapiens

<400> 68  
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gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
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aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcttttctg 840  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tcagaatcaa agacatgaac ttttaagcctc ttatcaatct tcgcagcctg gttatagctg 1140
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```

<210> 69  
 <211> 708  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
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 Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
 35 40 45  
 Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
 50 55 60  
 Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80  
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly  
 340 345 350  
 Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn  
 355 360 365  
 Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr  
 370 375 380  
 Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro  
 385 390 395 400  
 Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met  
 405 410 415  
 Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu  
 420 425 430  
 Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala  
 435 440 445  
 Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu  
 450 455 460  
 Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr  
 465 470 475 480

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys  
485 490 495

Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys  
500 505 510

Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys  
515 520 525

Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser  
530 535 540

Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr  
545 550 555 560

Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys  
565 570 575

Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys  
580 585 590

Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn  
595 600 605

Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn  
610 615 620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sapiens

<400> 70  
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agctgcagcc ttttgaacaa cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120  
ttaccacgct tggttgagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180  
gaatctggta gacctgtggt taacccgttc cctctccatg tgtctcctcc tacaaagttt 240  
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tcttcctcct gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420  
tgaaattttt aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480  
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgct 540  
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600  
aattgccaac aaccctggc actgcgactg tactctacag caagttctga ggagcatggc 660  
gtccaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttgg atgaacatgc 720



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tggcagacca ttcttcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaaac 780
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cctgccaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatagt 960
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tagatccatc tcactattta ataatgaaat ttattttttt aattttaaag caaataaaag 1260
cttaactttg aacctatgga aaaaaaaaaa aaaaaaaaaa aaaca 1305

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<210> 71  
 <211> 259  
 <212> PRT  
 <213> Homo sapiens

<400> 71  
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 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser

Thr Val Val

<210> 72  
<211> 2290  
<212> DNA  
<213> Homo sapiens

<400> 72  
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tgctgggctc agtgctgtca ggctcggcca cgggctgccc gccccgctgc gaggctccg 180  
cccaggaccg cgctgtgctg tgccaccgca agtgctttgt ggcagtcccc gagggcatcc 240  
ccaccgagac gcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300  
agttcgccag cttcccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360  
tggagccccg cgcttcaac aacctcttca acctcggac gctgggtctc cgcagcaacc 420  
gcctgaagct catcccgtca ggcgtcttca ctggcctcag caacctgacc aagcaggaca 480  
tcagcgagaa caagatcggt atcctactgg actacatggt tcaggacctg tacaacctca 540  
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aaaaaaaaaa 2290

<210> 73  
<211> 620  
<212> PRT  
<213> Homo sapiens

<400> 73  
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20 25 30

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
 35 40 45  
 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
 50 55 60  
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
 65 70 75 80  
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
 85 90 95  
 Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
 100 105 110  
 Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
 115 120 125  
 Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
 130 135 140  
 Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
 145 150 155 160  
 Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
 165 170 175  
 Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
 180 185 190  
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
 195 200 205  
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
 210 215 220  
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
 225 230 235 240  
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
 245 250 255  
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
 260 265 270  
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
 275 280 285  
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
 290 295 300  
 Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445

Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn  
 580 585 590

Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser  
 595 600 605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile  
 610 615 620

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 74

tcacctggag cctttattgg cc

22

<210> 75

<211> 23

<212> DNA

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 75

ataccagcta taaccaggct gcg

23

<210> 76

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg  
gg

50

52

<210> 77

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 77

ccatgtgtct cctcctacaa ag

22

<210> 78

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 78

gggaatagat gtgatctgat tgg

23

<210> 79

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 79

cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg

50

<210> 80

<211> 22

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 80

agcaaccgcc tgaagctcat cc

22

<210> 81

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 81

aaggcgcggt gaaagatgta gacg

24

<210> 82

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 82

gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga

50

<210> 83

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 83

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agccaggagag ccggccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180
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agccctggac atctgatgaa acagtgggtg ctggtggcac cgtggtgctc aagtgccaaag 300
tgaaagatca cgaggactca tccctgcaat ggtctaacc tgctcagcag actctctact 360
ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420
agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtac acctgctcaa 480
tcttcaactat gcctgtgcga actgccaagt ccctcgtcac tgtgctagga attccacaga 540
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gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaagggg gaccaagaac 660
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gccactactt gatccggcac aaaggaaact acctgcacac tgaggcaaaa ggctccgacg 1260
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ctcccgttg ctcccagcc caccacccc cctgtacaga atgtctgctt tgggtgcggt 1500
tttgtactcg gtttgaatg gggaggagg agggcgggg gaggggaggg ttgccctcag 1560

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaaacaaa 1680  
aaaca 1685

<210> 84  
<211> 398  
<212> PRT  
<213> Homo sapiens

<400> 84  
Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala  
1 5 10 15  
Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
20 25 30  
Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
35 40 45  
Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
50 55 60  
Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
65 70 75 80  
Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
85 90 95  
Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
100 105 110  
Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
115 120 125  
Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
130 135 140  
Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
145 150 155 160  
Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
165 170 175  
Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
180 185 190  
Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
195 200 205  
Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
210 215 220  
Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
225 230 235 240  
Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
245 250 255  
Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
260 265 270  
Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300  
 Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
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 Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335  
 Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350  
 His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365  
 Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380  
 Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 87

cctagcacag tgacgagggg cttggc

26

<210> 88

<211> 50

<212> DNA

<213> Artificial Sequence



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 88

aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 89

gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90

<211> 2755

<212> DNA

<213> Homo sapiens

<400> 90

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ggcttcggac	attggagcac	taaatgaact	tgaatttgtt	ctgtggcgag	caggatgggc	120
gctgttactt	tgtgatgaga	tcggggatga	attgctcgct	ttaaaaatgc	tgctttggat	180
tctgttgctg	gagacgtctc	tttgttttgc	cgctggaaac	gttacagggg	acgtttgcaa	240
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gcacaaccga aagggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460
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<210> 91  
 <211> 696  
 <212> PRT  
 <213> Homo sapiens

<400> 91  
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 1 5 10 15  
 Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn  
 20 25 30  
 Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
 35 40 45  
 Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
 50 55 60  
 Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn  
 65 70 75 80  
 Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
 85 90 95  
 Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380  
 Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
595 600 605

Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
610 615 620

Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
625 630 635 640

Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
645 650 655

Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr  
660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
675 680 685

Cys Gly Ser His Ser Leu Ser Asp  
690 695

<210> 92  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 92  
gttgatctg ggcaacaata ac 22

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 93  
attgttgatgc aggctgagtt taag 24

<210> 94  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 94  
ggtggctata catgtagc aattacctgg acacgctgtc ccggg 45

<210> 95  
<211> 2226  
<212> DNA  
<213> Homo sapiens

<400> 95

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tggccgctgg gcccgcgggg ggattccttg cagttggggg gtccgctcgg agcgaggggc 180
gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300
ggggcctcag agaattgaggc cggcgcttcg cctgtgcctc ctctggcagg cgctctggcc 360
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gttgat 2226

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<210> 96  
 <211> 490  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
 Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
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 20 25 30  
 Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45  
 Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60  
 Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80  
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335  
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln  
 340 345 350  
 Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala  
 355 360 365  
 Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr  
 370 375 380  
 Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe  
 385 390 395 400  
 Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr  
 405 410 415  
 Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln  
 420 425 430

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu  
435 440 445

Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val  
450 455 460

Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu  
465 470 475 480

Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala  
485 490

<210> 97  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 97  
tggaaggaga tgcgatgccca cctg 24

<210> 98  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 98  
tgaccagtgg ggaaggacag 20

<210> 99  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 99  
acagagcaga ggggtgccttg 20

<210> 100  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 100  
tcagggacaa gtggtgtctc tccc 24

<210> 101  
<211> 24  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 101

tcaggggaagg agtgtgcagt tctg

24

<210> 102

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 102

acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct

50

<210> 103

<211> 2026

<212> DNA

<213> Homo sapiens

<400> 103

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ctaaaagtgt	caagcgttga	cagcttgga	gcgtttattt	atacatctct	gtaaaaaggat	1860
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gtgttatttg	tttcaccttc	aagcctttgc	cctgagggtg	tacaatcttg	tcttgcgttt	1980
tctaaatcaa	tgcttaataa	aatattttta	aaggaaaaaa	aaaaaa		2026

<210> 104



## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

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Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
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Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
          20          25          30
Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
          35          40          45
Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
          50          55          60
Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
          65          70          75          80
Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
          85          90          95
His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
          100          105          110
Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
          115          120          125
Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
          130          135          140
Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
          145          150          155          160
Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
          165          170          175
Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
          180          185          190
Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
          195          200          205
Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
          210          215          220
Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
          225          230          235          240
Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
          245          250          255
Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
          260          265          270
Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
          275          280          285
Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
          290          295          300
Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly

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305						310						315					320
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Ser	Ile	Ile	Asn	Ile	Tyr	Lys	Glu	Gly	Asn	Leu	Ala	Ile	Gln	Gln	Ala		
			340					345					350				
Gly	Lys	Asn	Met	Ser	Ala	Arg	Leu	Thr	Val	Val	Cys	Lys	Gln	Cys	Pro		
		355					360					365					
Leu	Leu	Arg	Arg	Gly	Leu	Asn	Tyr	Ile	Ile	Met	Gly	Gln	Val	Gly	Glu		
	370					375					380						
Asp	Gly	Arg	Gly	Lys	Ile	Met	Pro	Asn	Ser	Phe	Ile	Met	Met	Phe	Lys		
385					390					395					400		
Thr	Lys	Asn	Gln	Lys	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Lys	Gln	Cys			
				405					410					415			

<210> 105  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 105  
ccgattcata gacctcgaga gt 22

<210> 106  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 106  
gtcaaggagt. cctccacaat ac 22

<210> 107  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 107  
gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt 45

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<210> 108
<211> 1838
<212> DNA
<213> Homo sapiens
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<400> 108  
cggacgcgtg ggcggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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ttcctttctcc gtggcctacg aggggtcccca gcctgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180
atctggctcc agccctctcc acctccccag tcttctcccc cgctcagcc ccatccgtgt 240
catacctgcc ggggactggt tgacagcttt aacaagggcc catccgggac 300
aactttggag gtggaacac tgccctgggag gaagagaatt tgtccaaata caaagacagt 360
gagaccgcgc ttgtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420
cgcttctggt agctgagtga ggagctgggt gagagctggt ggtttcacaa gcagcaggag 480
gccccggacc tcttccagtg gctgtgctca gattccctga agctctgctg ccccgagggc 540
accttcgggc cctcctgcct tccctgtcct gggggaacag agaggccctg cggtggtctac 600
gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660
tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720
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tcaaactgtt tgcaatgcaa gaagggtggt gccctgcatc acctcaagtg tntagacatt 840
gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgcgt gaacactgag 900
ggctcctatg agtgccgaga ctgtgccaa gctgcctag gctgcatggg ggcagggcca 960
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cagatcccgag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggtgctg 1200
cagcagatgt tctttggcat catcatctgt gcaactggcca cgctggctgc taaggcgac 1260
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gcccaggtac ccaggcccgg gcagacaagg cccctggggg aaaaagtagc cctgaagggtg 1560
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acaggggtgg ggccatcaca gctccctcct gccagctgca tgctgccagt tcctgttctg 1740
tgttcaccac atccccacac cccattgcca cttatttatt catctcagga aataaagaaa 1800
ggtcttgtaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

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&lt;210&gt; 109

&lt;211&gt; 420

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

```

Met Ala Pro Trp Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
 1             5             10             15
Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20             25             30
Pro Pro Pro Gln Ser Ser Pro Pro Gln Pro His Pro Cys His Thr
      35             40             45
Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50             55             60
Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
      65             70             75             80
Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
      85             90             95
Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
      100            105            110
Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
      115            120            125
Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
      130            135            140

```

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
145 150 155 160  
Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
165 170 175  
Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
180 185 190  
Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
195 200 205  
Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
210 215 220  
Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
225 230 235 240  
Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
245 250 255  
Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
260 265 270  
Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
275 280 285  
Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
290 295 300  
Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
305 310 315 320  
Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
325 330 335  
Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
340 345 350  
Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
355 360 365  
Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
370 375 380  
Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
385 390 395 400  
Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
405 410 415  
Ile Lys Gly Arg  
420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 110  
cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 111  
attctgcgtg aacactgagg gc 22

<210> 112  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 112  
atctgcttgt agccctcggc ac 22

<210> 113  
<211> 1616  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1461)..(1461)  
<223> a, t, c or g

<400> 113  
tgagaccctc ctgcagcctt ctcaagggag agccccactc tgcctcttgc tcctccaggg 60  
cagcaccatg cagccccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120  
cggggccgccc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
agaggtgccc accctggaca gggccgacat ggaggagctg gtcacccccca cccacgtgag 240  
ggcccagtag gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagagggt 300  
cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
gctggtgttc ggcattggagc agcggctgcc gcccaacagc gagctggtgc aggccgtgct 420  
gcggctcttc caggagccgg tccccaaggc cgcgctgcac aggcacgggc ggctgtcccc 480  
gcgcagcggc cgggcccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540  
ccgcacctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggcctt 600  
cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agccgctgct 660  
gctacagggt tcggtgcaga gggagcatct gggcccgcgt gcgtccggcg cccacaagct 720  
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cgagaactgg gtgctggagc ccccgggctt cctggcttat gactgtgtgg gcacctgccg 960  
gcagcccccg gaggccctgg ctttcaagtg gccgtttctg gggcctcgac agtgcacgcg 1020  
ctcggagact gactcgtcgc ccatgatcgt cagcatcaag gaggggaggca ggaccaggcc 1080  
ccaggtggtc agcctgcccc acatgagggt gcagaagtgc agctgtgcct cggatgggtc 1140  
gtcgtgcca aggaggctcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200  
gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260  
ggacaaatgc tctgtgctct ctagttagcc ctgaatttgc ttcctctgac aagttacctc 1320  
acctaatttt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380  
ttctctattc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500  
 aaagtcctcc accaccactc tggacctaag acctgggggtt aagtgtgggt tgtgcatccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45  
 Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335  
 Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350  
 Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115  
 aggactgccca taacttgccct g 21

<210> 116  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116  
 ataggagttg aagcagcgct gc 22

<210> 117  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117  
 tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118  
 <211> 1857  
 <212> DNA  
 <213> Homo sapiens

<400> 118  
 gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc gatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcataat tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180  
 aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tttgaccaag gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaaactggt atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgatg ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgccc 480
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc accttctgaa 540
tacacctggt tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600
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ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
agctcttgtt tgggagagca tagtaaat ttagagaact tgaagccaaa aggatttaaa 1620
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cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtgcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

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<210> 119  
 <211> 299  
 <212> PRT  
 <213> Homo sapiens

<400> 119  
 Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
 1 5 10 15  
 Leu Ala Ile Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
 20 25 30  
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
 35 40 45  
 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
 50 55 60  
 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 65 70 75 80  
 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
 85 90 95  
 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
165 170 175  
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
180 185 190  
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
195 200 205  
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
210 215 220  
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
225 230 235 240  
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
245 250 255  
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
260 265 270  
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
275 280 285  
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 121

tgatcgcat ggggacaaag gcgcaagctc gagaggaaac tggtgtgcct

50

<210> 122

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 122

acacctggtt caaagatggg

20

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 123  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 123  
taggaagagt tgctgaaggc acgg 24

<210> 124  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 124  
ttgccttact caggtgctac 20

<210> 125  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 125  
actcagcagt ggtaggaaag 20

<210> 126  
<211> 1210  
<212> DNA  
<213> Homo sapiens

<400> 126  
cagcgcgtgg ccggcgccgc tgtggggaca gcatgagcgg cggttggatg ggcgaggttg 60  
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctccgactag 120  
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180  
gctcaggctc gtgcccaccc accaagtacc agtgccgcac cagtggctta tgcgtgcccc 240  
tcacctggcg ctgcgacagg gacttggaact gcagcgatgg cagcgatgag gaggagtga 300  
ggattgagcc atgtaccag aaagggcaat gccaccgccc ccctggcctc ccctgccccct 360  
gcaccggcgt cagtgaactg tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420  
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
ggcgctgcga cgccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540  
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagt 600  
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtccccct 660  
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagccca actgcctatg 720  
gggttattgc agctgctgcg gtgctcagtg caagcctggc caccgccacc ctccctcttt 780  
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agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900  
ccgtcactca gccctgggag tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960  
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaacccgagc 1020  
tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080  
agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140  
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200

aagttgcttc

<210> 127  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 127  
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15  
Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30  
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45  
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60  
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80  
Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
85 90 95  
Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
100 105 110  
Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
115 120 125  
Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
130 135 140  
Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
145 150 155 160  
Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
165 170 175  
Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
180 185 190  
Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
195 200 205  
Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
210 215 220  
Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala  
225 230 235 240  
Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln  
245 250 255  
Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
260 265 270  
Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
275 280

<210> 128

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 128  
 aagttccagt gccgcaccag tggc 24  
  
 <210> 129  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 129  
 ttggttccac agccgagctc gtcg 24  
  
 <210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50  
  
 <210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> modified\_base  
 <222> (1837)..(1837)  
 <223> a, t, c or g  
  
 <400> 131  
 cccacgcgtc cgggtctcgct cgctcgcgca gcggcggcag cagaggtcgc gcacagatgc 60  
 gggttagact ggcgggggga ggaggcggag gaggggaagga agctgcatgc atgagaccca 120  
 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccgga 180  
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240  
 gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcggccct gcacagctca 300  
 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360  
 ggacccccag cggagggggt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420  
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatac 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgtc 600  
 atgaaggatt caagatccgg taccgcgacc tacacaatat ggtttcatta tgtcgcgatg 660  
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
 atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780  
 atcgctgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840  
 ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900  
 ctccaatggt gagtacgga gatttcgtct gccacccgcg gccttgtgag cgctacaacc 960  
 acggaactgt ggtggagttt tactgcatc ctggctacag cctcaccagc gactacaagt 1020

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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acatcacctg ccagtatgga gagtgggttc cttcttatca agtctactgc atcaaatacag 1080
agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaagatt gtggcggttca 1140
cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gacctgact 1260
ttgtggtggt agacggcggtg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320
gcttgagtgc cttaggcccc ggggtacatgg cctctgtggg ccagggtgc cccttaccg 1380
tggacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440
agtcagaaac ctgtgacagc gtctcaggct cttctgagct gtcctaaagt ctgtattcac 1500
ctcccagggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcattccatca tgcccactgg gtgttggttc 1620
taagaaactg attgattaaa aaatttccca aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cttttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtagaggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

```

<210> 132  
 <211> 490  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
 Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln  
 1 5 10 15  
 Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val  
 20 25 30  
 Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr  
 35 40 45  
 Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu  
 50 55 60  
 Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val  
 65 70 75 80  
 Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys  
 85 90 95  
 Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser  
 100 105 110  
 Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu  
 115 120 125  
 Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile  
 130 135 140  
 Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn  
 145 150 155 160  
 Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile  
 165 170 175  
 Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn  
 180 185 190  
 Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr  
 195 200 205  
 Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys  
 210 215 220

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu  
 225 230 235 240

Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe  
 245 250 255

Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val  
 260 265 270

Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr  
 275 280 285

Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys  
 290 295 300

Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr  
 305 310 315 320

Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu  
 325 330 335

Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His  
 340 345 350

Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe  
 355 360 365

Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala  
 370 375 380

Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val  
 385 390 395 400

Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr  
 405 410 415

Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys  
 420 425 430

Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro  
 435 440 445

Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile  
 450 455 460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 134  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134  
 agccaggatc gcagtaaaac tcc

23

<210> 135  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135  
 atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct

50

<210> 136  
 <211> 1815  
 <212> DNA  
 <213> Homo sapiens

<400> 136  
 cccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cgggccgtcg gtggcctaga 60  
 gatgctgctg ccgcgggttg agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120  
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtggggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tgggctgctg ggccgcgacg ggtcgctgc 240  
 tgagtgcctc ggatttggac ctgagaggag ggcagccagt ctgccgggga gggacacaga 300  
 ggccttgcta taaagtcatt tacttccatg atacttctcg aagactgaac tttaggaag 360  
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420  
 agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480  
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540  
 ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600  
 gcgaggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660  
 acatgttcca gtggaatgat gaccgggtgca acatgaagaa caatttcatt tgcaaatatt 720  
 ctgatgagaa accagcagtt ctttctagag aagctgaagg tgaggaaaca gagctgacaa 780  
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840  
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccct ctctctctcc 900  
 ttgtgggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960  
 cagaccctag cacaaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020  
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080  
 ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140  
 tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200  
 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260  
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320  
 aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380  
 ggaaaatata cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440  
 tccccacgac ctctgtgttg acccccacgt tttggctgta tcctttatcc cagccagtca 1500  
 tccagctcga ctttatgaga aggtaccttg cccaggctcg gcacatagta gactctcaat 1560  
 aaatgtcact tgggttgggtg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620  
 aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680  
 atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740  
 ttggcctgtg catcggcaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800  
 agcaggaaaa aaaaa 1815

<210> 137

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

```

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
 1          5          10          15
Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
          20          25          30
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
          35          40          45
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
          50          55          60
Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
          65          70          75          80
Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
          85          90          95
Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
          100          105          110
Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
          115          120          125
Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
          130          135          140
Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
          145          150          155          160
Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
          165          170          175
Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
          180          185          190
Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
          195          200          205
Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
          210          215          220
Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
          225          230          235          240
Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
          245          250          255
Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
          260          265          270
Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
          275          280          285
Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
          290          295          300
Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly

```



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

305                      310                      315                      320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
                                  325                      330                      335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
                                  340                      345                      350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
                                  355                      360                      365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
                                  370                      375                      380

<210> 138  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50.

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaacccgg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgtc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgtactg 240  
 cctgcaccag cggcggggtg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcgtg tttcgacacg gggctcggag 360  
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

```

ccccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600
tgtggaagac attccccttc tttcaccaac cttcaaccga caggaggtct ttattcggtc 660
cactaacatt tttcggaatc tggagtccac ccgttggttg ctggctgggc ttttccagtg 720
tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgatatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgcccctatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
cacatccttg tacatactgc ccaaggaaaga cagggaagt cttcagatgg cagtagggcc 1080
attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
caagatcaga aagctgtatc tctatgctgc tcatgatgtg accttcatac cgctcttaat 1200
gaccctgggg atttttgacc acaaattggcc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga ggtggcctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

```

&lt;210&gt; 142

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val  
1 5 10 15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala  
20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu  
35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro  
50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu  
65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu  
85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu  
100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly  
115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val  
130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe  
145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu  
165 170 175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
180 185 190

Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

195 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
oligonucleotide probe

<400> 144  
gcagctctat taccacggga agga 24

<210> 145  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145  
tccttcccgt ggtaatagag ctgc 24

<210> 146  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146  
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147  
<211> 1686  
<212> DNA  
<213> Homo sapiens

<400> 147  
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180  
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240  
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300  
agctgccagc ggaaccctta gtggtatttt gtatgagcca ccagcagaaa aagagcaaaa 360  
ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420  
agaagaagtt tatgattggt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480  
gagctctttc tccccagtc cagagggtgt caggctggct gacggccctg ggcattgcaa 540  
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600  
cctccgggcc gcaaagggtg tgtgccggca gctgggatgt gggagggtg tactgactca 660  
aaaacgctgc aacaagcatg cctatggccg aaaaccatc tggctgagcc agatgtcatg 720  
ctcaggacga gaagcaaccc ttcaggattg ccttcttggg ccttggggga agaacacctg 780  
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagttag 840  
aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgtat ggggctctgt 900  
ctgtgatgac aactggggag aaaaggagga ccagggtgta tgcaagcaac tgggctgtgg 960  
gaagtccctc tctccctcct tcagagaccg gaaatgctat ggccctgggg ttggccgcat 1020  
ctggctggat aatgttcgtt gctcagggga ggagcagtc ctggagcagt gccagcacag 1080  
attttggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgtg 1140  
ggtgggcatc atctaactctg ttgagtgcct gaatagaaga aaaacacaga agaagggagc 1200  
atttactgtc tacatgactg catgggatga acactgatct tcttctgccc ttggactggg 1260  
acttatactt ggtgccccctg attctcaggc cttcagagtt ggatcagaac ttacaacatc 1320  
aggtctagtt ctcaggcctg cagacatagt ttggaactac atcaccacct ttcctatgtc 1380  
tccacattgc acacagcaga ttcccagcct ccataattgt gtgtatcaac tacttaaata 1440  
cattctcaca cacacacaca cacacacaca cacacacaca ccatttgtcc 1500  
tgtttctctg aagaactctg acaaaatata gattttggta ctgaaagaga ttctagagga 1560  
acggaatttt aaggataaat tttctgaatt ggttatgggg tttctgaaat tggctctata 1620  
atctaattag atataaaatt ctggttaactt tatttacaat aataaagata gcactatgtg 1680

ttcaaa

<210> 148  
<211> 347  
<212> PRT  
<213> Homo sapiens

<400> 148

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Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
 1           5           10           15
Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
          20           25           30
Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
          35           40           45
Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
          50           55           60
Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
          65           70           75           80
Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
          85           90           95
Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
          100          105          110
Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
          115          120          125
Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
          130          135          140
Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
          145          150          155          160
Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
          165          170          175
Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
          180          185          190
Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
          195          200          205
Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
          210          215          220
Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
          225          230          235          240
Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
          245          250          255
Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
          260          265          270
Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
          275          280          285
Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly

```

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

290

295

300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 149

ttcagctcat caccttcacc tgcc

24

<210> 150

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 150

ggctcataca aaataccact aggg

24

<210> 151

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

<210> 152

<211> 1427

<212> DNA

<213> Homo sapiens

<400> 152

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60  
acccacgcgt ccgcggacgc gtgggcggaac gcgtgggccc gctaccagga agagtctgcc 120  
gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180  
cctgggcgtc ttccggcctc tccggctgct gcagtgggtg cgcggaagg cctacctgcg 240  
gaatgctgtg gtgggtgatca caggcgccac ctgagggtg ggcaaagaat gtgcaaaagt 300  
cttctatgct gcgggtgcta aactgggtgct ctgtggcccg aatgggtggg ccctagaaga 360  
gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420  
ggtgaccttc gacctcacag actctggggc catagtgtgca gcagcagctg agatcctgca 480  
gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540  
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

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tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
gcacgcaacc caggctttct ttgactgtct gcgtgcccag atggaacagt atgaaattga 780
ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaatg ccatcaccgc 840
ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900
ggtggccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
cttactgcct tccttggtcg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080
agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc caggggtgag 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttggccgcc atggccaac ttgtttattg cagcttataa tggttac 1427

```

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

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Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
 1           5           10           15
Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
          20           25           30
Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
          35           40           45
Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
          50           55           60
Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
          65           70           75           80
Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
          85           90           95
Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
          100          105          110
Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
          115          120          125
Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
          130          135          140
Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
          145          150          155          160
Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
          165          170          175
Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
          180          185          190
Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
          195          200          205
Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr
          210          215          220

```

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg  
225 230 235 240

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu  
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val  
260 265 270

Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu  
275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu  
290 295 300

Arg Lys Ser Lys Asn Ser  
305 310

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 154

ggtgctaaac tgggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156

tcatactgtt ccatctcggc acgc

24

<210> 157

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;400&gt; 157

aatggtggtg ccctagaaga gctcatcaga gaactcaccg cttctcatgc

50

&lt;210&gt; 158

&lt;211&gt; 1771

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 158

```

cccacgcgtc cgctggtggtt agatcgagca accctctaaa agcagtttag agtggtataaa 60
aaaaaaaaaa acacaccaaa cgctcgagc cacaaaaggg atgaaatttc ttctggacat 120
cctcctgctt ctcccgttac tgatcgctg ctccctagag tccttcgtga agctttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcggtgctg attacaggag ctgggcatgg 240
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaaggt 360
tcataacctt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420
gaaggcagaa attggagatg ttagtatttt agtaataaat gctggtgtag tctatacatc 480
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720
aataaactga gtcaaaaaca catgtctgtg tcctaatttc gtaaactctg gcttcatcaa 780
aaatccaagt acaagtttgg gaccactctt ggaacctgag gaagtggtaa acaggctgat 840
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtgt 960
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080
cttctgtttt ttctaattat cccatttctt tcaatatcat ttttgaggct ttggcagttc 1140
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200
tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac tttattaaaa 1260
taatttccaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320
ttattttaaca tatattttta tttttgattg cacttaaat tttgtataatt tgtgtttctt 1380
tttctgttct acataaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440
tagtggtatt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500
gccactctgt ttcctgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560
gctagaggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620
agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a aaaaaaaaaa 1771

```

&lt;210&gt; 159

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

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Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val
 1           5           10           15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
          20          25          30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
      35          40          45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
 50          55          60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
 65          70          75          80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
      85          90          95

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
130 135 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr  
145 150 155 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
245 250 255

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 161

atcccatgca tcagcctgtt tacc

24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 162  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 162  
gctggtgtag tctatacatc agatttgttt gctacacaag atcctcag 48

<210> 163  
<211> 2076  
<212> DNA  
<213> Homo sapiens

<400> 163  
cccacgcgtc cgccggacgcg tgggtcgact agttctagat cgccgagcggc cgccccgcggc 60  
tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaggtg 120  
attgtttcgc tggtcctggt gatgcctggc cctgtgatg ggctgtttcg ctccctatac 180  
agaagtgttt ccatgccacc taaggagagc tcaggacagc cattatttct caccctttac 240  
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300  
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360  
ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420  
caggggtggc cgggagggtt atccatgttt ggactctttg tggacatgg gccttatgtt 480  
gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540  
ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600  
gcagtcaatg aggacgatgt agcacgggat ttatacagt cactaattca gtttttccag 660  
atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720  
tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
aacctgaacg gaattgctat tggagatgga tattctgata ccgaatcaat tatagggggc 840  
tatgcagaat tcctgtacca aattggcctt ttggatgaga agcaaaaaaa gtacttccag 900  
aagcagtgcc atgaatgcat agaacacatc aggaagcaga actggtttga ggcctttgaa 960  
atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020  
acaggatgta gtaattacta taactttttg cgggtgcacg aacctgagga tcagctttac 1080  
tatgtgaaat ttttgtcact cccagagggt agacaagcca tccacgtggg gaatcagact 1140  
tttaattgat gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200  
ccatggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260  
atcatcgtgg cagctgccct gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320  
caggaatata agaaggcaga aaaaaaagtt tggagatct ttaaatctga cagtgaagtg 1380  
gctggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440  
attttaccct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500  
aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagaggtttt 1560  
cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620  
tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680  
ttttgggggg agatgtttac tacaaaatta acatgagtac atgagtaaga attacattat 1740  
ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800  
ttttagggtc ttgaatagga agttttaatt tcttctaaga gtaagtgaag agtgcagttg 1860  
taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920  
gtgttttgaa atattattgg ataagaatag ctcaattatc ccaataaat ggatgaagct 1980  
ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040  
gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164  
<211> 476  
<212> PRT  
<213> Homo sapiens

<400> 164  
Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
1 5 10 15

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
                   20                  25                  30  
 Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
                   35                  40                  45  
 Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
           50                  55                  60  
 Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val  
   65                  70                  75                  80  
 Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln  
                   85                  90                  95  
 Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro  
                  100                 105                 110  
 Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val  
          115                 120                 125  
 Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr  
   130                 135                 140  
 Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser  
  145                 150                 155                 160  
 Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala  
                  165                 170                 175  
 Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu  
                  180                 185                 190  
 Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys  
          195                 200                 205  
 Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg  
   210                 215                 220  
 Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser  
  225                 230                 235                 240  
 Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile  
                  245                 250                 255  
 Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His  
          260                 265  
 Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu  
   275                 280                 285  
 Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr  
  290                 295                 300  
 Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys  
  305                 310                 315                 320  
 Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro  
          325                 330                 335  
 Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly  
          340                 345                 350

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365  
Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
370 375 380  
Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400  
Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415  
Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430  
Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
435 440 445  
Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460  
Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

<210> 165  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165  
ttccatgccca cctaagggag actc

24

<210> 166  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166  
tgcatgaggt gtgcaatggc tggc

24

<210> 167  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 167  
agctctcaga ggctgggtcat aggg

24

<210> 168  
<211> 50

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

&lt;210&gt; 169

&lt;211&gt; 2477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

cgagggcttt	tccggctccg	gaatggcaca	tgtgggaatc	ccagtcttgt	tggctacaac	60
atttttccct	ttcctaacaa	gttctaacag	ctgttctaac	agctagtgat	caggggttct	120
tcttgctgga	gaagaaaggg	ctgagggcag	agcagggcac	tctcactcag	ggtgaccagc	180
tccttgccctc	tctgtggata	acagagcatg	agaaagtga	gagatgcagc	ggagtgaagg	240
gatggaagtc	taaaatagga	aggaattttg	tgtgcaatat	cagactctgg	gagcagttga	300
cctggagagc	ctgggggagg	gcctgcctaa	caagctttca	aaaaacagga	gcgacttcca	360
ctgggctggg	ataagacgtg	ccggtaggat	aggggaagact	gggttttagtc	ctaatatcaa	420
attgactggc	tgggtgaact	tcaacagcct	tttaacctct	ctgggagatg	aaaacgatgg	480
cttaaggggc	cagaaataga	gatgctttgt	aaaataaaat	tttaaaaaaa	gcaagtattt	540
tatagcataa	aggctagaga	ccaaaataga	taacaggatt	ccctgaacat	tcctaagagg	600
gagaaagtat	gttaaaaata	gaaaaaccaa	aatgcagaag	gaggagactc	acagagctaa	660
accaggatgg	ggaccctggg	tcaggccagc	ctctttgctc	ctcccggaaa	ttatttttgg	720
tctgaccact	ctgccttgtg	ttttgcagaa	tcattgtgag	gcccaaccgg	gaagggtggg	780
cagatgagca	cacacaggag	ccgtctcctc	accgccgccc	ctctcagcat	ggaacagagg	840
cagccctggc	cccgggccct	ggaggtggac	agccgctctg	tggtcctgct	ctcagtgggc	900
tgggtgctgc	tggccccccc	agcagccggc	atgcctcagt	tcagcacctt	ccactctgag	960
aatcgtgact	ggaccttcaa	ccacttgacc	gtccaccaag	ggacgggggc	cgtctatgtg	1020
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acagggccag	aagaggacaa	caagtctcgt	taccgcgcc	tcattcgtga	gccctgcagc	1140
gaagtgtcta	ccctcaccaa	caatgtcaac	aagctgtcta	tcattgacta	ctctgagaac	1200
cgcctgctgg	cctgtgggag	cctctaccag	ggggtctgca	agctgctgca	gctggatgac	1260
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cgagaccctg	agtcctcagc	catgctcgac	tatgagctac	acagcgattt	tgtctcctct	1500
ctcatcaaga	tcccttcaga	caccctggcc	ctggtctccc	actttgacat	cttctacatc	1560
tacggctttg	ctagtggggg	ctttgtctac	tttctcactg	tccagcccga	gacccctgag	1620
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cagtatcacc	acccgcccga	tgactctgcc	ctgtgtgcct	tccctatccg	ggccatcaac	1920
ttgcagatca	aggagcgcct	gcagtcctgc	taccagggcg	agggcaacct	ggagctcaac	1980
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tgtggactgg	acatcaacca	gcccctggga	ggctcaactc	cagtggagg	cctgaccctg	2100
tacaccacca	gcagggaccg	catgacctct	gtggcctcct	acgtttacaa	cggctacagc	2160
gtggtttttg	tggggactaa	gagtggcaag	ctgaaaaagg	taagagtcta	tgagttcaga	2220
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agatttaact	ataggcaact	ttattttctt	ggggaacaaa	ggtgaaatgg	ggaggtaaga	2340
aggggttaat	tttgtgactt	agcttctagc	tacttctctc	agccatcagt	cattgggtat	2400
gtaaggaatg	caagcgtatt	tcaatatttc	ccaaacttta	agaaaaaact	ttaagaaggt	2460
acatctgcaa	aagcaaa					2477

&lt;210&gt; 170

&lt;211&gt; 552

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;400&gt; 170

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Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
 1           5           10           15
Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
           20           25           30
Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
           35           40           45
Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
           50           55           60
Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
           65           70           75           80
Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
           85           90           95
Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
           100          105          110
Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
           115          120          125
Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
           130          135          140
Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
           145          150          155          160
Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
           165          170          175
Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
           180          185          190
Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
           195          200          205
Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
           210          215          220
Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
           225          230          235          240
Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
           245          250          255
Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
           260          265          270
Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
           275          280          285
Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
           290          295          300
Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
           305          310          315          320
Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg

```

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
340 345 350  
Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
355 360 365  
Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
370 375 380  
Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
385 390 395 400  
His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
405 410 415  
Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
420 425 430  
Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
435 440 445  
Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn  
450 455 460  
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
465 470 475 480  
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
485 490 495  
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
500 505 510  
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
515 520 525  
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
530 535 540  
Leu Tyr Phe Leu Gly Glu Gln Arg  
545 550

<210> 171  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171  
tggaataaccg cctcctgcag

20

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>



<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

24

<210> 173  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

43

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<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens
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<220>
<221> modified_base
<222> (1683)..(1683)
<223> a, t, c or g
```

<400>	174					
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aacacgcgat	g	gaccacgtg	g	agcctccgg	g	gcgacgctg
tgctggctcgt	c	cttgggcttc	c	ctggtgctcc	g	ctggagcacc
tgcggctccg	c	ccatcgacag	c	ctggggctgc	a	ctggaacttc
attccacctt	c	ctggatcttc	c	gtggggctcca	t	ccgtgtgcc
ggagggaccg	c	ctgtctaag	a	atgaaggcct	g	caccttcacc
cgtggaacct	g	gcatgagcca	g	gaaagaggca	a	ctctgggaac
aggccttcgt	c	cctgatggcc	g	gcagagatcg	g	gattctgcgt
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tgaggcttag	g	gacaacttac	a	aaggcgctta	c	ggacctttat
tgatgtccag	g	ggtggtgcc	c	ctccagctaca	a	acctatcatt
tggagaatga	a	atatggttcc	t	tataataaag	a	catgccctac
cactggagga	c	ccgtggcatt	g	gtggaactgc	t	agacaacaag
gcaaggggat	t	tgtccaggga	g	gtcttgcca	c	gcagtcaaca
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actggacggg	g	gtggtttgac	t	ctgtggggag	g	tatcttgat
ttttgaaaac	c	cggtctgcgc	a	ttgttgagc	c	catcaacctc
acggaggcac	c	caactttggc	t	ttcatgaatg	g	cttccatgac
atgtcaccag	c	ctatgactat	g	gatgctgtgc	t	cggcgattac
acatgaagct	t	tcgagacttc	t	ttcggctcca	t	ccctctccct
accttcttcc	c	caagatggcc	t	tatgagccct	c	cttgtacctg
acgccctcaa	g	gtacctgggg	g	ggaccaatca	g	gcccatcaac
tgccagtcaa	t	tgggggaaat	g	ggacagtcct	t	tctctatgag
cctcgtctgg	c	catcctcagt	g	ggccacgtgc	g	gcagggtgtt
tatccatagg	a	attcttggac	t	tacaagacaa	t	tgccccctg
acaccgtgct	t	gaggatcttg	g	gtggagaatc	g	caactatggg
atgaccagcg	c	caaaggctta	a	attggaatc	t	tgattacccc
tcagaatcta	t	tgcctgtgat	a	atgaagaaga	g	gaggttcggc
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gctccacgcc	t	ttgtgacacc	t	tttctgaagc	g	ggagaagggg
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cggtggcacc	c	ccctcctgct	g	ggtgccagtg	g	gcctcctctt
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						300
						360
						420
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						780
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						1680
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						1800
						1860
						1920
						1980
						2040

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

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ctggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcagg 2100
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ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttg 2220
aggctgtcgg gctgtctcta ggggtggagc agctaatac atcgcccagc ctttggcc 2280
cagaaaaagt gctgaaacgt gcccttgac cggacgtcac agccctgcga gcatctg 2340
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catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga agccatgg 2760
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gaagtgtgtc caagtcgcga tttgagcctt gttctggggc ccagcccaac acctgggt 3060
ggctcactgt cctgagttgc agtaaagcta taacctgaa tcacaa 3106

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<210> 175  
 <211> 636  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MOD\_RES  
 <222> (539)  
 <223> Any amino acid

<400> 175  
 Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu  
 1 5 10 15  
 Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp  
 20 25 30  
 Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln  
 35 40 45  
 Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe  
 50 55 60  
 Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp  
 65 70 75 80  
 Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr  
 85 90 95  
 Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser  
 100 105 110  
 Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly  
 115 120 125  
 Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp  
 130 135 140  
 Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430  
 Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
 435 440 445  
 Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
 450 455 460  
 Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
 465 470 475 480  
 Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
 485 490 495  
 Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
 500 505 510

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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ccctgggtgag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120
aaggggagca aagccgggct cggcccagg cccccaggac ctccatctcc caatgttga 180
ggaatccgac acgtgacggg ctgtccgccg tctcagacta gaggagcgct gtaaacgcca 240
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tgctttgggc cgaccggcct ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480
atgtgccttg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaaacct gttggtcata ctgagaccag 600
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ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720
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ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960
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ctgtgtcagc tgtaaccaaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140
tgtacatgtt ccatggagggt accaactttg gatattggaa tgggtgccgat aagaagggac 1200
gcttccttcc gattactacc agctatgact atgatgcacc tatacttgaa gcagggggacc 1260
ccacacctaa gctttttgct cttcgagatg tcatcagcaa gttccaggaa gttcctttgg 1320
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ggcatttact ggctttccta gacttgcttt gcccccgagg gccattcat tcaatcttgc 1440
caatgacctt tgaggctgtc aagcaggacc atggcttcat gttgtaccga acctatatga 1500
cccataccat ttttgagcca acaccattct gggtgccaaa taatggagtc catgaccgtg 1560
cctatgtgat ggtggatggg gtgttccagg gtgttgtgga gcgaaatatg agagacaaac 1620
tatttttgac ggggaaactg ggttccaaac tggatatctt ggtggagaac atggggaggc 1680
tcagctttgg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740
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ggtttccctt ccagtggcca aaatggccat atcctcaagc tccttctggc cccacattct 1860
actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920
ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

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aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100
agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
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ggtggctcat gcctgtaatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280
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ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggagggtgt accactgcac 2460
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<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

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Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
 1          5          10          15
Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
          20          25          30
Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
          35          40          45
Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
          50          55          60
Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
          65          70          75          80
Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
          85          90          95
Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
          100          105          110
Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
          115          120          125
Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
          130          135          140
Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
          145          150          155          160
Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
          165          170          175
Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
          180          185          190
Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
          195          200          205
Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
          210          215          220
Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro
          225          230          235          240
Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
          245          250          255

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
                   260                                  265                                  270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
                   275                                  280                                  285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
                   290                                  295                                  300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
   305                                  310                                  315                                  320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
                                   325                                  330                                  335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile  
                                   340                                  345                                  350  
 Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro  
                   355                                  360                                  365  
 Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu  
                   370                                  375                                  380  
 Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu  
   385                                  390                                  395                                  400  
 Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr  
                                   405                                  410                                  415  
 Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val  
                                   420                                  425                                  430  
 Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val  
                   435                                  440                                  445  
 Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr  
                   450                                  455                                  460  
 Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg  
   465                                  470                                  475                                  480  
 Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro  
                                   485                                  490                                  495  
 Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu  
                                   500                                  505                                  510  
 Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys  
                   515                                  520                                  525  
 Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr  
                   530                                  535                                  540  
 Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly  
   545                                  550                                  555                                  560  
 Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr  
                                   565                                  570                                  575  
 Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu  
                   580                                  585                                  590

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu  
 595 600 605  
 Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu  
 610 615 620  
 Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640  
 Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178  
 tggctactcc aagaccctgg catg 24

<210> 179  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179  
 tggacaaatc cccttgctca gccc 24

<210> 180  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180  
 gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg 50

<210> 181  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181  
 ccagctatga ctatgatgca cc 22

<210> 182  
 <211> 24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182

tggcaccag aatggtgttg gctc

24

<210> 183

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183

cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc

50

<210> 184

<211> 1947

<212> DNA

<213> Homo sapiens

<400> 184

gctttgaaca	cgtctgcaag	cccaaagttg	agcatctgat	tggttatgag	gtatttgagt	60
gcaccacaa	tatggcttac	atgttgaaaa	agcttctcat	cagttacata	tccattat	120
gtgtttatg	ctttatctgc	ctctacactc	tcttctggtt	attcaggata	cctttgaagg	180
aatattcttt	cgaaaaagtc	agagaagaga	gcagtttttag	tgacattcca	gatgtcaaaa	240
acgattttgc	gttccttctt	cacatggtag	accagtatga	ccagctatat	tccaagcgtt	300
ttggtgtgtt	cttgtcagaa	gttagtgaaa	ataaaccttag	ggaaattagt	ttgaaccatg	360
agtggacatt	tgaaaaactc	aggcagcaca	tttcacgcaa	cgcccaggac	aagcaggagt	420
tgcatctgtt	catgctgtcg	ggggtgcccg	atgctgtctt	tgacctcaca	gacctggatg	480
tgctaaagct	tgaactaatt	ccagaagcta	aaattcctgc	taagatttct	caaatagacta	540
acctccaaga	gctccacctc	tgccactgcc	ctgcaaaaagt	tgaacagact	gcttttagct	600
ttcttcgcga	tcacttgaga	tgcccttcacg	tgaagttcac	tgatgtggct	gaaattcctg	660
cttgggtgta	tttctcaaaa	aaccttcgag	agttgtactt	aataggcaat	ttgaactctg	720
aaaacaataa	gatgatagga	cttgaatctc	tccgagagtt	gcggcacctt	aagattctcc	780
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caaagttagt	cattcataat	gacggcacta	aactcttggt	actgaacagc	cttaagaaaa	900
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ttttcagcct	ctctaattta	caggaactgg	atttaaagtc	caataacatt	cgcacaattg	1020
aggaaatcat	cagtttccag	cattttaaacc	gactgacttg	ttttaaatta	tggcataaca	1080
aaattgttac	tattcctccc	tctattaccc	atgtcaaaaa	cttggagtca	ctttatttct	1140
ctaacaacaa	gctcgaatcc	ttaccagtgg	cagtatttag	tttacagaaa	ctcagatgct	1200
tagatgtgag	ctacaacaac	atttcaatga	ttccaataga	aataggattg	cttcagaacc	1260
tgacagcatt	gcataatcact	gggaacaaag	tggaacattct	gccaaaacaa	ttgtttaaat	1320
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tttttgatac	cctgccactc	gaagtcaaa	aggcattgaa	tcaagacata	aatattccct	1560
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cttttaaaat	aaaacagaga	ggatgcatag	aaggctgata	gaagacataa	ctgaatgttc	1740
aatgtttgta	gggttttaag	tcattcattt	ccaaatcatt	tttttttttc	ttttggggaa	1800
aggggaaggaa	aaattataat	cactaatctt	ggttcttttt	aaattgtttg	taacttggat	1860
gctgcccgtc	ctgaatgttt	acaaattgct	tgccctgctaa	agtaaattgat	taaattgaca	1920
ttttcttact	aaaaaaaaaa	aaaaaaa				1947

<210> 185



## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile  
 1 5 10 15  
 Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg  
 20 25 30  
 Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser  
 35 40 45  
 Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His  
 50 55 60  
 Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe  
 65 70 75 80  
 Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His  
 85 90 95  
 Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln  
 100 105 110  
 Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala  
 115 120 125  
 Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro  
 130 135 140  
 Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu  
 145 150 155 160  
 Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser  
 165 170 175  
 Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val  
 180 185 190  
 Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
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[illegible]

<210> 186  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 186  
cctccctcta ttacccatgt c 21

<210> 187  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 187  
gaccaacttt ctctgggagt gagg 24

**<210> 188**

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe

&lt;400&gt; 188

gtcactttat ttctctaaca acaagctcga atccttacca gtggcag

47

&lt;210&gt; 189

&lt;211&gt; 2917

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

```

cccacgcgtc cggccttctc tctggacttt gcattttccat tccttttcat tgacaaaactg 60
acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120
aagacatttg tgttttacac acataaggat ctgtgttttg ggtttcttct tcctcccctg 180
acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240
gcactttatc gcctaggtac atcgaagtct ttgacctc atacagtgat tatgcctgtc 300
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cacaacccag acaaggtgtg gtgggccaag aacagccagg ccaaaccat tgccacggag 480
tcttgtcctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540
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agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgcagggaac 720
cagctgctgg agatccctac agagagcttc cactgggggc aacctttcca ggaaggagtt 780
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gctgatgtaa cacagagctc ataaaagctg tcggtcctta aggctgcccc gcgccttgcc 960
aaaatggagc ttgtaagaag gctcatgcca ttgacctct taattctctc ctgtttggcg 1020
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tggacaatag aaagaccaga aaacaaaagc atcagaatta tcttttcta tgtccagctt 1200
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gtcttctact acttcttctc tctaacatc tctattccaa actgtggcgg ttacctggat 1440
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aacttgcaac taaaagaccc aacttgacga ccaaaattat caaatgttgt ggaattttct 1920
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aatataatca cttttctgc atctcaact tctgaagtga tcaccgctca gaaacaactc 2040
cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100
gaagatgatg taatacaaaag tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160
tttgaatcca attcatttga aaagactata ctggaatcac catattatgt ggatttgaac 2220
caaactcttt ttgttcaagt tagtctgcac acctcagatc caaatttggt ggtgtttctt 2280
gatacctgta gagcctctcc cacctctgac ttgtcatctc caacctacga cctaatacaag 2340
agtggatgta gtcgagatga aacttgatga agtgcctcct tatttggaac ctatgggaga 2400
ttccagttta atgcctttaa attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460
gttttgatat gtgatagcag tgaccaccag tctcgtgca atcaagggtg tgtctccaga 2520
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ctgaaaaggg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcgga 2640
gaaactccaa accagccttt caacagtgtg catctgtttt cttcatgggt tctagctctg 2700
aatgtggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
 aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgtttc 2820  
 tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
 ggcctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

<210> 190  
 <211> 607  
 <212> PRT  
 <213> Homo sapiens

<400> 190  
 Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15  
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30  
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80  
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110  
 Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
290 295 300  
Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
305 310 315 320  
Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
325 330 335  
Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
340 345 350  
Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
355 360 365  
His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
370 375 380  
Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
385 390 395 400  
Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
405 410 415  
Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
420 425 430  
Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
435 440 445  
Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
450 455 460  
Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
465 470 475 480  
Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
485 490 495  
Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
500 505 510  
Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
515 520 525  
Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
530 535 540  
Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
545 550 555 560  
Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val  
565 570 575  
Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe  
580 585 590  
Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr  
595 600 605

<210> 191

<211> 21

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe

&lt;400&gt; 191

tctctattcc aaactgtggc g

21

&lt;210&gt; 192

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe

&lt;400&gt; 192

tttgatgacg attcgaaggt gg

22

&lt;210&gt; 193

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe

&lt;400&gt; 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc

47

&lt;210&gt; 194

&lt;211&gt; 2362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

gacggaagaa	cagcgctccc	gaggccgcgg	gagcctgcag	agaggacagc	cggcctgcgc	60
cgggacatgc	ggccccagga	gctccccagg	ctcgcgttcc	cgttgctgct	gttgctgttg	120
ctgctgctgc	cgccgcccgc	gtgccctgcc	cacagcgcca	cgcgcttcga	ccccacctgg	180
gagtccttgg	acgcccgcga	gctgcccgcg	tggtttgacc	aggccaagtt	cggcatcttc	240
atccactggg	gagtgttttc	cgtgcccagc	ttcggtagcg	agtggttctg	gtggatttgg	300
caaaaggaaa	agataccgaa	gtatgtggaa	tttatgaaaag	ataattaccc	tcctagtttc	360
aaatatgaag	attttgacc	actatttaca	gcaaaatttt	ttaatgcaa	ccagtgggca	420
gatatttttc	aggcctctgg	tgccaaatac	attgtcttaa	cttccaaaca	tcatgaaggc	480
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440
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atgtctaagg ctaggaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560
aactggataa gaaaattatt tggcagttca gccctttccc tttttccac taaatttttc 1620
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cattgatttg tttccatgtg tgactcagag gtgagaattt tttcacatta tagtagcaag 1740
gaattgggtg tattatggac cgaactgaaa attttatgtt gaagccatat ccccatgat 1800
tatatagtta tgcatactt aatatgggga tttttctgg gaaatgcatt gctagtcaat 1860
ttttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920
cacacctaata gtgtatggta tagactgttg ctcttaggct acagacatat acagcatgtt 1980
actgaatact gtaggcaata gtaacagtgg tatttgtata tcgaaacata tggaaacata 2040
gagaaggtag agtaaaaata ctgtaaaata aatggtgcac ctgtataggg cacttaccac 2100
gaatggagct tacaggactg gaagtgtctc tgggtgagtc agtgagtga tgtgaaggcc 2160
taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220
ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280
caaacgtttt aatttttaaa acctttttgg ctcttttgta ataacactta gcttaaaaca 2340
taaactcatt gtgcaaatgt aa 2362

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<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu  
1 5 10 15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr  
20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala  
35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
180 185 190

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
195 200 205

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220

Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
 450 455 460

Asn Val Ile  
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196

tggtttgacc aggccaaagtt cgg



## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 197  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 197  
 ggattcatcc tcaaggaaga gcgg 24  
  
 <210> 198  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 198  
 aacttgacgc atcagccact ctgc 24  
  
 <210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 199  
 ttccgtgccc agcttcggta gcgagtgggt ctggtgggtat tggca 45  
  
 <210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 200  
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 gtccagaaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120  
 catctgaggt gtttccctgg ctctgaaggg gtaggcacga tggccagggtg cttcagcctg 180  
 gtgttgcttc tcaattccat ctggaccacg aggtcctctg tccaaggctc ttgctgtgca 240  
 gaagagcttt ccattccagg gtcattgcaga attatgggga tcacccttgt gagcaaaaag 300  
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360  
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420  
 ggctggggtg gagatggatt cgtgggtcatc tctaggatta gcccaaacc caagtgtggg 480  
 aaaaatgggg tgggtgtcct gatttggaag gttccagtga gccgacagtt tgcagcctat 540  
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600  
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcacag 660  
 acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgct 720  
 ccagcttcca ctctatttcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780  
 gaaactagca ccatgtctac agaaactgaa ccatttggtg aaaataaagc agcattcaag 840  
 aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900  
 ttgtgtgctg cagtgtgtct tggattttgc tatgtcaaaa ggtagtgtaa ggccttcctt 960  
 tttacaataa agaatacaga gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020  
 gccaatgata gcaaccctaa tgaggaaatc aagaaaactg ataaaaacc agaagagtcc 1080  
 aagagtccaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140  
 tgaggagaca cacctgaggc tggtttcttt catgctcctt accctgcccc agctggggaa 1200  
 atcaaaaggg ccaaagaacc aaagaagaaa gtccaccctt ggttcctaac tggaatcagc 1260

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320
cctgtctgga tcctatcctc ctacctccaa agcttcccac ggcctttcta gcctggctat 1380
gtcctaataa tatccactg ggagaaagga gttttgcaa gtgcaaggac ctaaaacatc 1440
tcatacgtat ccagtggtaa aaaggcctcc tggctgtctg aggctagggt ggttgaaagc 1500
caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac cttttcttca 1560
gctctgaaag agaaacacgt atcccacctg acatgtcctt ctgagcccgg taagagcaaa 1620
agaatggcag aaaagttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740
gcagggactg taaacacaga cagggtcaaa gtgttttctc tgaacacatt gagttggaat 1800
cactgtttag aacacacaca cttacttttt ctggctctcta ccactgctga tattttctct 1860
aggaatatata cttttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920
gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040
tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct gggaagctat 2100
ttttttcagt tttgatattt ctagcttatc tacttccaaa ctaattttta tttttgctga 2160
gactaatctt attcattttc tctaattatg taaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca cattttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaagggg ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaac tt 2372

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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr  
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Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile  
20 25 30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys  
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile  
130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
145 150 155 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
165 170 175

Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

180 185 190  
Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
195 200 205  
Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
210 215 220  
Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
225 230 235 240  
Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
245 250 255  
Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
260 265 270  
Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
275 280 285  
Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
290 295 300  
Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
305 310 315 320  
Glu Val

<210> 202  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202  
gagctttcca tccaggtgtc atgc 24

<210> 203  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 203  
gtcagtgaca gtacctactc gg 22

<210> 204  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 204

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tggagcagga ggagtagtag tagg

24

&lt;210&gt; 205

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 205

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

&lt;210&gt; 206

&lt;211&gt; 1620

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (973)..(973)

&lt;223&gt; a, t, c or g

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (977)..(977)

&lt;223&gt; a, t, c or g

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (996)..(996)

&lt;223&gt; a, t, c or g

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (1003)..(1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

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agatggcggg cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgtcttc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccacccaacg cgaagacggg aaccctgtgt 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat ttcatgttt agtaaagtgg 300
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tggagttctt tgccaattgg tctaattgact gccaatcatt tgcccctatc tatgctgacc 540
tctcccttaa atacaactgt acagggctaa attttgggaa ggtggatgtt ggacgctata 600
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tgatcctgtt ccaaggtggc aaggaggcaa tgcggcgggc acagattgac aagaaaggac 720
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agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccttaa gcccttctgg cttcgtttat ggtcttcatt aaaagtataa 1380

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gcctaacttt gtcgctagtc ctaaggagaa acccttaacc acaaagtttt tatcattgaa 1440  
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggccttgag 1500  
actttccttt gtgtggtagg acttggagga gaaatcccct ggactttcac taaccctctg 1560  
acatactccc cacaccagtg tgatggcttt ccgtaataaa aagattggga tttccttttg 1620

<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg  
1 5 10 15  
Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu  
20 25 30  
Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly  
35 40 45  
Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg  
50 55 60  
Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn  
65 70 75 80  
Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
85 90 95  
Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
100 105 110  
Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
115 120 125  
Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
130 135 140  
Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
145 150 155 160  
Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
165 170 175  
Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
180 185 190  
Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
195 200 205  
Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
210 215 220  
Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
225 230 235 240  
Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
245 250 255  
Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
260 265 270  
Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser

Asp Gly Glu Asn Lys Lys Asp Lys  
290 295

<210> 208  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 208  
gcttgatat tcgcatgggc ctac 24

<210> 209  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 209  
tggagacaat atccctgagg 20

<210> 210  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 210  
aacagttggc cacagcatgg cagg 24

<210> 211  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 211  
ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
<211> 1985  
<212> DNA  
<213> Homo sapiens

<400> 212  
ggacagctcg cggcccccca gagctctagc cgctcaggag ctgcctgggg acgtttgccc 60  
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cccattgctc ctgctgcccc gctcctacgg actgcccttc tacaacggct tctactactc 180  
caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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ggtcattgac gggctggagg atgaaagcgg tctggtggag ctggagctgc ggggtgtggt 600
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gaagaagagg gcctcggggg cctccggagc tgggctttgg gcctctcctg cccacctcta 1620
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aggggcccct aggtgtgtgt actttggaca ataaatggtg ctatgactgc cttccgccaa 1860
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaa

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&lt;210&gt; 213

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 213

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Met Gly Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr
  1             5             10             15
Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
             20             25             30
Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
             35             40             45
Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
             50             55             60
Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
             65             70             75             80
Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
             85             90             95
Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
             100            105            110
Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp
             115            120            125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr
             130            135            140

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu  
145 150 155 160  
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg  
165 170 175  
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala  
180 185 190  
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly  
195 200 205  
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr  
210 215 220  
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro  
225 230 235 240  
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp  
245 250 255  
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu  
260 265 270  
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu  
275 280 285  
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys  
290 295 300  
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser  
305 310 315 320  
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu  
325 330 335  
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr  
340 345 350  
Gly Val Tyr Cys Tyr Arg Gln His  
355 360

<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 215  
ttcccttggtg ggttgagg 18

<210> 216  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216  
agggctggaa gccagttc 18

<210> 217  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217  
agccagtggg gaaatgag 18

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218  
tgtccaaagt acacacacct gagg 24

<210> 219  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 219  
gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
<211> 1503  
<212> DNA  
<213> Homo sapiens

<400> 220  
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tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgcca 180  
cgggaaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240  
ccaactcacc ccagaggaaa gccaggcccg tctggggcgg atcgtggacc gcatggaccg 300

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

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cgacgggctgt gtgggttggg aggagctgag caacgccacc tatggccact acgcgcccgg 480
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aaa 1503

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<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
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 20 25 30  
 Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala  
 35 40 45  
 His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val  
 50 55 60  
 Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu  
 65 70 75 80  
 Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp  
 85 90 95  
 Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg  
 100 105 110  
 His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp  
 115 120 125  
 Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly  
 130 135 140  
 His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr  
 145 150 155 160  
 Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp  
 165 170 175  
 Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu  
 180 185 190

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr  
195 200 205  
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu  
210 215 220  
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala  
225 230 235 240  
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn  
245 250 255  
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro  
260 265 270  
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu  
275 280 285  
Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
290 295 300  
Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
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325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 225  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 225  
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<210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
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 atcctgggct tcgctcgatt tgccgcccag gcgcctccca gacctagagg ggcgctggcc 240  
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 gcggggctct gaggaggtga cgcgcggggc ctcccgacc ctggccttgc ccgcattctc 360  
 cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgacgcctgg atccccggctc 420  
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 tccagtctca aatgctttct agatggctct cttctttcac agtaactaaa ggcaaaagta 780  
 gtacacagga ggccacagga caagcagtgt ccacagcaca tccaccaaca ggtaaacgac 840  
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 tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 960  
 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc ctgtttcaag 1020  
 ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080  
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 aaa 2403

<210> 227  
 <211> 550

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> PRT

<213> Homo sapiens

<400> 227

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Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu
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Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
          20          25          30
Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
          35          40          45
Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
          50          55          60
Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
          65          70          75          80
Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
          85          90          95
Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
          100          105          110
Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
          115          120          125
Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
          130          135          140
Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
          145          150          155          160
Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
          165          170          175
Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
          180          185          190
Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
          195          200          205
Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
          210          215          220
Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
          225          230          235          240
Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
          245          250          255
Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
          260          265          270
Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
          275          280          285
Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
          290          295          300
Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
          305          310          315          320

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
530 535 540

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2c1.txt

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 229  
 ctgctgtcca caggggag 18

<210> 230  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 230  
 ccttgaagca tactgctc 18

<210> 231  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 231  
 gagatagcaa tttccgcc 18

<210> 232  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232  
 ttcctcaaga gggcagcc 18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233  
 cttggcacca atgtccgaga tttc 24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 234  
gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235  
<211> 2586  
<212> DNA  
<213> Homo sapiens

<400> 235  
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cctgcagaaa cagtacttag gtaattgtag ggcgaggatt ataaatgaaa tttgcaaaat 2280  
cacttagcag caactgaaga caattatcaa ccacgtggag aaaatcaaac cgagcagggc 2340  
tgtgtgaaac atggttgtaa tatgcgactg cgaacactga actctacgcc actccacaaa 2400  
tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt tcttaaagtt 2460  
taaagttgca catgattgta taagcatgct ttctttgagt tttaaattat gtataaacat 2520  
aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580  
aaaaaa 2586

<210> 236  
<211> 350  
<212> PRT  
<213> Homo sapiens

<400> 236  
Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala  
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val	Pro	Thr	Ala 20	Pro	Ala	Pro	Ala	Pro 25	Thr	Ala	Thr	Ser	Ala 30	Pro	Val
Lys	Pro	Gly 35	Pro	Ala	Leu	Ser	Tyr 40	Pro	Gln	Glu	Glu	Ala 45	Thr	Leu	Asn
Glu	Met 50	Phe	Arg	Glu	Val	Glu 55	Glu	Leu	Met	Glu	Asp 60	Thr	Gln	His	Lys
Leu 65	Arg	Ser	Ala	Val	Glu 70	Glu	Met	Glu	Ala	Glu 75	Glu	Ala	Ala	Ala	Lys 80
Ala	Ser	Ser	Glu	Val 85	Asn	Leu	Ala	Asn	Leu 90	Pro	Pro	Ser	Tyr	His 95	Asn
Glu	Thr	Asn	Thr 100	Asp	Thr	Lys	Val	Gly 105	Asn	Asn	Thr	Ile	His 110	Val	His
Arg	Glu	Ile 115	His	Lys	Ile	Thr	Asn 120	Asn	Gln	Thr	Gly	Gln 125	Met	Val	Phe
Ser	Glu 130	Thr	Val	Ile	Thr	Ser 135	Val	Gly	Asp	Glu	Glu 140	Gly	Arg	Arg	Ser
His 145	Glu	Cys	Ile	Ile	Asp 150	Glu	Asp	Cys	Gly	Pro 155	Ser	Met	Tyr	Cys	Gln 160
Phe	Ala	Ser	Phe	Gln 165	Tyr	Thr	Cys	Gln	Pro 170	Cys	Arg	Gly	Gln	Arg 175	Met
Leu	Cys	Thr	Arg 180	Asp	Ser	Glu	Cys	Cys 185	Gly	Asp	Gln	Leu	Cys 190	Val	Trp
Gly	His	Cys 195	Thr	Lys	Met	Ala	Thr 200	Arg	Gly	Ser	Asn	Gly 205	Thr	Ile	Cys
Asp	Asn 210	Gln	Arg	Asp	Cys	Gln 215	Pro	Gly	Leu	Cys	Cys 220	Ala	Phe	Gln	Arg
Gly 225	Leu	Leu	Phe	Pro	Val 230	Cys	Thr	Pro	Leu	Pro 235	Val	Glu	Gly	Glu	Leu 240
Cys	His	Asp	Pro	Ala 245	Ser	Arg	Leu	Leu	Asp 250	Leu	Ile	Thr	Trp	Glu 255	Leu
Glu	Pro	Asp	Gly 260	Ala	Leu	Asp	Arg	Cys 265	Pro	Cys	Ala	Ser	Gly 270	Leu	Leu
Cys	Gln	Pro 275	His	Ser	His	Ser	Leu 280	Val	Tyr	Val	Cys	Lys 285	Pro	Thr	Phe
Val	Gly 290	Ser	Arg	Asp	Gln	Asp 295	Gly	Glu	Ile	Leu	Leu 300	Pro	Arg	Glu	Val
Pro 305	Asp	Glu	Tyr	Glu	Val 310	Gly	Ser	Phe	Met	Glu 315	Glu	Val	Arg	Gln	Glu 320
Leu	Glu	Asp	Leu	Glu 325	Arg	Ser	Leu	Thr	Glu 330	Glu	Met	Ala	Leu	Gly 335	Glu
Pro	Ala	Ala	Ala 340	Ala	Ala	Ala	Leu	Leu 345	Gly	Gly	Glu	Glu	Ile 350		

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 237  
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 <223> Synthetic oligonucleotide probe  
  
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 <210> 238  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Synthetic Oligonucleotide Probe  
  
 <400> 238  
 ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49  
  
 <210> 239  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Synthetic Oligonucleotide Probe  
  
 <400> 239  
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 <223> Synthetic Oligonucleotide Probe  
  
 <400> 240  
 ttggcagctt catggagg 18  
  
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 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Synthetic Oligonucleotide Probe  
  
 <400> 241  
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 <210> 242  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 242  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 243  
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<212> DNA  
<213> Homo Sapien

<400> 244  
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cactctcctt ccctcccaaa cacacatgtg catgtacaca cacacataca 150  
cacacataca ccttcctctc cttcactgaa gactcacagt cactcactct 200  
gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcttggcc 250  
attacctctg cagctccttt ggcttggtga gtcaaaaaaac atgggagggg 300  
ccaggcacgg tgactcacac ctgtaatccc agcattttgg gagaccgagg 350  
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agaaaccccc atctctacta aaaatacaaa aattagccag gagtggtggc 450  
agggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 tacctggcca atctcacaga gctggacctg tcccagaaca gcttttcgga 1200  
 tgcccgagac tgtgatttcc atgccctgcc ccagctgctg agcctgcacc 1250  
 tagaggagaa ccagctgacc cggctggagg accacagctt tgcagggctg 1300  
 gccagcctac aggaactcta tctcaaccac aaccagctct accgcatcgc 1350  
 cccaggggcc ttttctggcc tcagcaactt gctgcggctg cacctcaact 1400  
 ccaacctcct gagggccatt gacagccgct ggtttgaaat gctgccaac 1450  
 ttggagatac tcatgattgg cggcaacaag gtagatgcca tcctggacat 1500  
 gaacttccgg cccctggcca acctgcgtag cctggtgcta gcaggcatga 1550  
 acctgcggga gatctccgac tatgccctgg aggggctgca aagcctggag 1600  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 ccttagggga tcgtcctggg ctcatcgcca tcctggctct cgctgtcctt 2800  
 ctcctggcag ctgggctagc ggcccacctt ggcacaggcc aacccaggaa 2850  
 ggggtgtgggt gggaggcggc ctctccctcc agcctgggct ttctggggct 2900  
 ggagtgcccc ttctgtccgg gttgtgtctg ctcccctcgt cctgccctgg 2950  
 aatccaggga ggaagctgcc cagatcctca gaaggggaga cactgttgcc 3000  
 accattgtct caaaattctt gaagctcagc ctgttctcag cagtagagaa 3050  
 atcactagga ctacttttta ccaaaagaga agcagtctgg gccagatgcc 3100  
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 aagttgccct tacctcctag ggtcacctct gctgccattc tgaggaacat 3250  
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 ggcattccga agctgacttt ctataggcaa tttgtacct ttgtggagaa 3600  
 atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650  
 aataaaaata aataataaca ataaaaaaa 3679

<210> 245  
 <211> 713  
 <212> PRT  
 <213> Homo Sapien

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 Ala Thr Ala Thr Val Pro Val Val Pro Trp His Val Pro Cys Pro  
                   20                  25                  30  
 Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser  
                   35                  40                  45  
 Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu  
                   50                  55                  60  
 Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu  
                   65                  70                  75

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
				80					85					90
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
				95					100					105
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
				110					115					120
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
				125					130					135
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
				140					145					150
Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser
				155					160					165
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile
				170					175					180
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met
				185					190					195
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg
				200					205					210
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu
				215					220					225
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu
				230					235					240
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg
				245					250					255
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys
				260					265					270
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu
				275					280					285
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser
				290					295					300
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu
				305					310					315
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala
				320					325					330
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn
				335					340					345
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn
				350					355					360
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys
				365					370					375
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile
				380					385					390

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg
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Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys
				410					415					420
Leu	Pro	Leu	Ile	Ser	Pro	Arg	Ser	Phe	Pro	Pro	Ser	Leu	Gln	Val
				425					430					435
Ala	Ser	Gly	Glu	Ser	Met	Val	Leu	His	Cys	Arg	Ala	Leu	Ala	Glu
				440					445					450
Pro	Glu	Pro	Glu	Ile	Tyr	Trp	Val	Thr	Pro	Ala	Gly	Leu	Arg	Leu
				455					460					465
Thr	Pro	Ala	His	Ala	Gly	Arg	Arg	Tyr	Arg	Val	Tyr	Pro	Glu	Gly
				470					475					480
Thr	Leu	Glu	Leu	Arg	Arg	Val	Thr	Ala	Glu	Glu	Ala	Gly	Leu	Tyr
				485					490					495
Thr	Cys	Val	Ala	Gln	Asn	Leu	Val	Gly	Ala	Asp	Thr	Lys	Thr	Val
				500					505					510
Ser	Val	Val	Val	Gly	Arg	Ala	Leu	Leu	Gln	Pro	Gly	Arg	Asp	Glu
				515					520					525
Gly	Gln	Gly	Leu	Glu	Leu	Arg	Val	Gln	Glu	Thr	His	Pro	Tyr	His
				530					535					540
Ile	Leu	Leu	Ser	Trp	Val	Thr	Pro	Pro	Asn	Thr	Val	Ser	Thr	Asn
				545					550					555
Leu	Thr	Trp	Ser	Ser	Ala	Ser	Ser	Leu	Arg	Gly	Gln	Gly	Ala	Thr
				560					565					570
Ala	Leu	Ala	Arg	Leu	Pro	Arg	Gly	Thr	His	Ser	Tyr	Asn	Ile	Thr
				575					580					585
Arg	Leu	Leu	Gln	Ala	Thr	Glu	Tyr	Trp	Ala	Cys	Leu	Gln	Val	Ala
				590					595					600
Phe	Ala	Asp	Ala	His	Thr	Gln	Leu	Ala	Cys	Val	Trp	Ala	Arg	Thr
				605					610					615
Lys	Glu	Ala	Thr	Ser	Cys	His	Arg	Ala	Leu	Gly	Asp	Arg	Pro	Gly
				620					625					630
Leu	Ile	Ala	Ile	Leu	Ala	Leu	Ala	Val	Leu	Leu	Leu	Ala	Ala	Gly
				635					640					645
Leu	Ala	Ala	His	Leu	Gly	Thr	Gly	Gln	Pro	Arg	Lys	Gly	Val	Gly
				650					655					660
Gly	Arg	Arg	Pro	Leu	Pro	Pro	Ala	Trp	Ala	Phe	Trp	Gly	Trp	Ser
				665					670					675
Ala	Pro	Ser	Val	Arg	Val	Val	Ser	Ala	Pro	Leu	Val	Leu	Pro	Trp
				680					685					690
Asn	Pro	Gly	Arg	Lys	Leu	Pro	Arg	Ser	Ser	Glu	Gly	Glu	Thr	Leu
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<223> Synthetic Oligonucleotide Probe

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<210> 247  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 247  
aaacttgtag atggagacca gctc 24

<210> 248  
<211> 45  
<212> DNA  
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<400> 248  
aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249  
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<212> DNA  
<213> Homo Sapien

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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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ccctgacact gtgtttgacc tgggtggagct ggaggtcctc aagctggagc 650  
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aaggagctgt ggctctacca cacagcggcc aagattgaag cgcctgcgct 750  
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agcaagtctc aagagcgcag tatttgata atcagggctt cctccctgga 2000  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

agataactta tacattccca agaaagttca gcccagatgg aagggtgttca 2150  
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 ggcatttaac acccacctgg acttcagcag agtgggtccg ggcgaaccag 2250  
 ccatgggacg gtcacccagc agtgccgggc tgggctctgc ggtgcggtcc 2300  
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 ggagtctcag ggcaggggtg cagtttccct tgagcaaagc agccagacgt 2550  
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a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met Arg Gln Thr Ile Ile Lys Val Ile Lys Phe Ile Leu Ile Ile

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

1	5	10	15
Cys Tyr Thr Val	Tyr Tyr Val His Asn Ile Lys Phe Asp Val	Asp	
	20	25	30
Cys Thr Val Asp	Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg		
	35	40	45
Cys Ala His Pro	Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe		
	50	55	60
Tyr Ile Ser Leu	Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr		
	65	70	75
Leu Trp Trp Met	Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu		
	80	85	90
Ser Ile Arg Glu	Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys		
	95	100	105
Asn Asp Phe Ala	Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro		
	110	115	120
Leu Tyr Ser Lys	Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu		
	125	130	135
Asn Lys Leu Arg	Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp		
	140	145	150
Lys Leu Arg Gln	Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
	155	160	165
Leu His Leu Phe	Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
	170	175	180
Leu Val Glu Leu	Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
	185	190	195
Thr Ile Pro Pro	Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
	200	205	210
Trp Leu Tyr His	Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
	215	220	225
Phe Leu Arg Glu	Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp		
	230	235	240
Ile Lys Glu Ile	Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu		
	245	250	255
Glu Leu His Leu	Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
	260	265	270
Ile Val Ile Asp	Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
	275	280	285
Arg Leu Lys Ser	Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp		
	290	295	300
Val Gly Val His	Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
	305	310	315

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr  
320 325 330

Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser  
335 340 345

Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn  
350 355 360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His  
365 370 375

Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile  
380 385 390

Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu  
395 400 405

Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys  
410 415 420

Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe  
425 430 435

Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala  
440 445 450

Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln  
455 460 465

Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln  
470 475 480

Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile  
485 490 495

Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly  
500 505 510

Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp  
515 520 525

Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg  
530 535 540

Ala Asp Lys Glu Gln Ala  
545

<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

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<210> 252

<211> 24

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

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 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200  
 ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250  
 ggcttcaggg cgggtccaggc gggttctagca ctggatttgg aaactttgag 300  
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350  
 ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400  
 gttatgtgaa tggtagtggt gcctatgcc aaggacctggc tatgggtggct 450  
 tcagacatga tgggttctct gaagaccttc ttcagttgcc acaaagaatt 500  
 ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550  
 cagctggcat tgggtctagag ctttataagg ccattcagcg agggaccatc 600  
 aagtgcaact ttgcgggggt tgccttgagg gattcctgga tctcccctgt 650  
 tgattcggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700  
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 gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800  
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 taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900  
 cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950  
 agatgcctta agccagctca tgaatggccc catcagaaag aagctcaaaa 1000

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100  
 gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150  
 tcgtagatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200  
 gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250  
 taaatctttg gaaacatctg cttttgtcaa gtcctacaag aaccttgctt 1300  
 tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350  
 atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400  
 gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450  
 cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500  
 gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550  
 ggaggcaatt tggaatttat ttctgcttct taaaaaaacc taagattttt 1600  
 taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255  
 <211> 452  
 <212> PRT  
 <213> Homo Sapien

<400> 255  
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 Leu Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp  
 20 25 30  
 Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val  
 35 40 45  
 Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn  
 50 55 60  
 Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln  
 65 70 75  
 Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu  
 80 85 90  
 Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp  
 95 100 105  
 Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr  
 110 115 120  
 Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu  
 125 130 135  
 Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe  
 140 145 150

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser  
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 170 175 180  
 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly  
 185 190 195  
 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu  
 200 205 210  
 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys  
 215 220 225  
 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala  
 230 235 240  
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys  
 245 250 255  
 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr  
 260 265 270  
 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser  
 275 280 285  
 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His  
 290 295 300  
 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly  
 305 310 315  
 Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp  
 320 325 330  
 Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe  
 335 340 345  
 Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly  
 350 355 360  
 Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp  
 365 370 375  
 Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu  
 380 385 390  
 Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp  
 395 400 405  
 Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn  
 410 415 420  
 Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser  
 425 430 435  
 Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln  
 440 445 450

Gln Glu

&lt;210&gt; 256

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttgccc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgaacc tgctcagcca ccgctgggca 250
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cctcgctacc tggggaattc accctatgac attgccttgg tgaagctgtc 450
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ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

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Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg
 1           5           10           15

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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser

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20

25

30

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Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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50                               55                               60
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65                               70                               75
Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
80                               85                               90
Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
95                               100                              105
Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
110                              115                              120
Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
125                              130                              135
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
140                              145                              150
Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
155                              160                              165
Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
170                              175                              180
Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
185                              190                              195
Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
200                              205                              210
Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
215                              220                              225
Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
230                              235                              240
Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
245                              250                              255
Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
260                              265                              270
Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
275                              280                              285
Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
290                              295                              300
Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
305                              310

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<210> 258  
 <211> 2427  
 <212> DNA  
 <213> Homo Sapien

<400> 258  
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 Page 133

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200  
 gaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatcccagct 250  
 ctctcaata cggaaaatac ctgaccctag agaattgtgg tgatctggtg 300  
 aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350  
 cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400  
 ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagtttcat 450  
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 gagcacagga tccttagtgg ccgccccct cttggctttc tcaaccaag 1550  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
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 gtcccctgcc ctgaagctgg cagttcagtc ccttattctg ccctgttgga 1800  
 agccctgctg aaccctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aaccctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgctcc 1900  
 atcatactca ggtctcccta ctctgcctt agattcctca ataagatgct 1950  
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<210> 259  
 <211> 556  
 <212> PRT  
 <213> Homo Sapien

<400> 259  
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 Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu  
 35 40 45  
 Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg  
 50 55 60  
 Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln  
 65 70 75  
 Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg  
 80 85 90  
 Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala  
 95 100 105  
 Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu  
 110 115 120

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Thr Cys Trp Leu	Ser 125	Ile Arg Gln Ala	Glu 130	Leu Leu Leu Pro	Gly 135
Ala Glu Phe His	His 140	Tyr Val Gly Gly	Pro 145	Thr Glu Thr His	Val 150
Val Arg Ser Pro	His 155	Pro Tyr Gln Leu	Pro 160	Gln Ala Leu Ala	Pro 165
His Val Asp Phe	Val 170	Gly Gly Leu His	Arg 175	Phe Pro Pro Thr	Ser 180
Ser Leu Arg Gln	Arg 185	Pro Glu Pro Gln	Val 190	Thr Gly Thr Val	Gly 195
Leu His Leu Gly	Val 200	Thr Pro Ser Val	Ile 205	Arg Lys Arg Tyr	Asn 210
Leu Thr Ser Gln	Asp 215	Val Gly Ser Gly	Thr 220	Ser Asn Asn Ser	Gln 225
Ala Cys Ala Gln	Phe 230	Leu Glu Gln Tyr	Phe 235	His Asp Ser Asp	Leu 240
Ala Gln Phe Met	Arg 245	Leu Phe Gly Gly	Asn 250	Phe Ala His Gln	Ala 255
Ser Val Ala Arg	Val 260	Val Gly Gln Gln	Gly 265	Arg Gly Arg Ala	Gly 270
Ile Glu Ala Ser	Leu 275	Asp Val Gln Tyr	Leu 280	Met Ser Ala Gly	Ala 285
Asn Ile Ser Thr	Trp 290	Val Tyr Ser Ser	Pro 295	Gly Arg His Glu	Gly 300
Gln Glu Pro Phe	Leu 305	Gln Trp Leu Met	Leu 310	Leu Ser Asn Glu	Ser 315
Ala Leu Pro His	Val 320	His Thr Val Ser	Tyr 325	Gly Asp Asp Glu	Asp 330
Ser Leu Ser Ser	Ala 335	Tyr Ile Gln Arg	Val 340	Asn Thr Glu Leu	Met 345
Lys Ala Ala Ala	Arg 350	Gly Leu Thr Leu	Leu 355	Phe Ala Ser Gly	Asp 360
Ser Gly Ala Gly	Cys 365	Trp Ser Val Ser	Gly 370	Arg His Gln Phe	Arg 375
Pro Thr Phe Pro	Ala 380	Ser Ser Pro Tyr	Val 385	Thr Thr Val Gly	Gly 390
Thr Ser Phe Gln	Glu 395	Pro Phe Leu Ile	Thr 400	Asn Glu Ile Val	Asp 405
Tyr Ile Ser Gly	Gly 410	Gly Phe Ser Asn	Val 415	Phe Pro Arg Pro	Ser 420
Tyr Gln Glu Glu	Ala 425	Val Thr Lys Phe	Leu 430	Ser Ser Ser Pro	His 435

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro
				440					445					450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg
				455					460					465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val
				470					475					480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser
				485					490					495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln
				500					505					510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser
				515					520					525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro
				530					535					540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu
				545					550					555

Cys

<210> 260  
 <211> 1638  
 <212> DNA  
 <213> Homo Sapien

<400> 260  
 gccgcgcgct ctctcccggc gcccacacct gtctgagcgg cgcagcgagc 50  
 cgcgccccgg gcgggctgct cggcgcggaa cagtgtctcg catggcaggg 100  
 attccagggc tcctcttctt tctcttcttt ctgctctgtg ctgttgggca 150  
 agtgagccct tacagtgcc cctggaaacc cacttggcct gcataccgcc 200  
 tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250  
 ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300  
 taagggaaact cactgcccc cttacgaaga ggccaagcaa tatctgtctt 350  
 atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400  
 tacatcctca gcagtagtgg agatggggcc caacaccgag actcaggggtc 450  
 ttcaggaaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500  
 tcagcatttt tgggaaggac ttcctgtctca actacccttt ctcaacatca 550  
 gtgaagttat ccacgggctg caccggcacc ctggtggcag agaagcatgt 600  
 cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650  
 cccagaagct tcgagtgggc ttcctaaagc ccaagtttaa agatgggtgt 700  
 cgaggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gtggatccgg gtgaaacgca cccatgtgcc caaggggttg atcaaggga 800  
atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850  
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctcttgctaa 900  
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950  
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000  
ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctggggt 1050  
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100  
ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
gatttcaacg tggctgtcag aatcactcct ctcaaatatg cccagatttg 1200  
ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250  
ttccctcctg gcagcaatta agggctcttca tgttcttatt ttaggagagg 1300  
ccaaattggt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400  
tgactggctt tactatttga aaactggttt gtgtatcata tcatatatca 1450  
tttaagcagt ttgaaggcat acttttgcac agaaataaaa aaaatactga 1500  
tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550  
caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
atatttgga tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261  
<211> 383  
<212> PRT  
<213> Homo Sapien

<400> 261  
Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu  
1 5 10 15  
Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro  
20 25 30  
Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr  
35 40 45  
Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu  
50 55 60  
Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu  
65 70 75  
Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu  
80 85 90  
Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile  
95 100 105

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Ser Ser Ser	Gly 110	Asp Gly Ala Gln	His 115	Arg Asp Ser Gly	Ser 120
Ser Gly Lys Ser	Arg 125	Arg Lys Arg Gln	Ile 130	Tyr Gly Tyr Asp	Ser 135
Arg Phe Ser Ile	Phe 140	Gly Lys Asp Phe	Leu 145	Leu Asn Tyr Pro	Phe 150
Ser Thr Ser Val	Lys 155	Leu Ser Thr Gly	Cys 160	Thr Gly Thr Leu	Val 165
Ala Glu Lys His	Val 170	Leu Thr Ala Ala	His 175	Cys Ile His Asp	Gly 180
Lys Thr Tyr Val	Lys 185	Gly Thr Gln Lys	Leu 190	Arg Val Gly Phe	Leu 195
Lys Pro Lys Phe	Lys 200	Asp Gly Gly Arg	Gly 205	Ala Asn Asp Ser	Thr 210
Ser Ala Met Pro	Glu 215	Gln Met Lys Phe	Gln 220	Trp Ile Arg Val	Lys 225
Arg Thr His Val	Pro 230	Lys Gly Trp Ile	Lys 235	Gly Asn Ala Asn	Asp 240
Ile Gly Met Asp	Tyr 245	Asp Tyr Ala Leu	Leu 250	Glu Leu Lys Lys	Pro 255
His Lys Arg Lys	Phe 260	Met Lys Ile Gly	Val 265	Ser Pro Pro Ala	Lys 270
Gln Leu Pro Gly	Gly 275	Arg Ile His Phe	Ser 280	Gly Tyr Asp Asn	Asp 285
Arg Pro Gly Asn	Leu 290	Val Tyr Arg Phe	Cys 295	Asp Val Lys Asp	Glu 300
Thr Tyr Asp Leu	Leu 305	Tyr Gln Gln Cys	Asp 310	Ala Gln Pro Gly	Ala 315
Ser Gly Ser Gly	Val 320	Tyr Val Arg Met	Trp 325	Lys Arg Gln Gln	Gln 330
Lys Trp Glu Arg	Lys 335	Ile Ile Gly Ile	Phe 340	Ser Gly His Gln	Trp 345
Val Asp Met Asn	Gly 350	Ser Pro Gln Asp	Phe 355	Asn Val Ala Val	Arg 360
Ile Thr Pro Leu	Lys 365	Tyr Ala Gln Ile	Cys 370	Tyr Trp Ile Lys	Gly 375
Asn Tyr Leu Asp	Cys 380	Arg Glu Gly			

<210> 262  
 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;400&gt; 262

gcatcgccct gggctctctcg agcctgctgc ctgctcccc gccccaccag 50  
ccatggtggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100  
accttcacct ccctgctgct gctggcgtcg acagccatcc tcaatgcggc 150  
caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300  
ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350  
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
cggctccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450  
ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgct 500  
ccatacagtt ctgagagcgg gtcctgcca tctgcctacc tgatgcctct 550  
atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600  
ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650  
ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700  
ggacagggac ccatcactga ggacatgctg tgtgccggct acttgagggg 750  
ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850  
gccgagcgca acaggccccg ggtctacatc agcctctctg cgcaccgctc 900  
ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950  
ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000  
tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgccgta 1100  
aataggctca tctacctcta cctctggggg cccggacggc tgctgcggaa 1150  
aggaaacccc ctccccgacc cgcccagcgg cctcaggccc ccctccaagg 1200  
catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttccggc 1250  
ccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300  
ataggatttt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350  
ataaattatt tattctccaa aaaaaaaa 1378

&lt;210&gt; 263

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 263



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	
Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu	185	190	195	
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His	200	205	210	
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met	215	220	225	
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly	230	235	240	
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu	245	250	255	
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn	260	265	270	
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val	275	280	285	
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly	290	295	300	
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala	305	310	315	

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gtcc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 266

agctctagac caatgccagc ttcc 24

<210> 267

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 267

gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 268

ggggaattca ccctatgaca ttgcc 25

<210> 269

<211> 24

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Synthetic Oligonucleotide Probe

<400> 269

gaatgccctg caagcatcaa ctgg 24

<210> 270

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 270

gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 271

gcggaagggc agaatgggac tccaag 26

<210> 272

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 272

cagccctgcc acatgtgc 18

<210> 273

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 273

tactgggtgg tcagcaac 18

<210> 274

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 274

ggcgaagagc agggtgagac cccg 24

<210> 275

<211> 45

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
gggcagggat tccagggctc c 21

<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcaggttc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcatcgcatc gctggtagag caag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 280

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
ttacagtgcc ccctggaaac ccacttgcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gtcctataca gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggag actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaagggtcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgtttga tggaggagct gcacaacctc taccgggccc 150

aggatatccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200

ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250

caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300

gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350

tacaacctca gcgcccgcac ctgcagccca ggccagatgt gcggccacta 400

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cacgcaggtg gtatgggcca agacagagag gatcggctgt ggttcccact 450  
tctgtgagaa gctccaggggt gttgaggaga ccaacatcga attactgggtg 500  
tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550  
ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600  
tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650  
gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700  
aatgggtact ctttcttccc tagcaacggg gattccggct ttcttggtaa 750  
cagaggtctc aggctcccctg gcaaccaagg ctctgcctgc tgtggaaacc 800  
caggcccca cttccttagc aacgaaagac ccgccctcca tggcaacaga 850  
ggctccacct tgcgtaacaa ctgaggtccc ttccattttg gcagctcaca 900  
gcctgccctc cttggatgag gagccagtta cttcccccaa atcgacccat 950  
gttcctatcc caaaatcagc agacaaaagt acagacaaaa caaaagtgcc 1000  
ctctaggagc ccagagaact ctctggacct caagatgtcc ctgacagggg 1050  
caagggaact cctaccccat gccaggagg aggctgaggc tgaggctgag 1100  
ttgcctcctt ccagtgaggt cttggcctca gtttttccag cccaggacaa 1150  
gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200  
agtccctgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250  
gggcgtgccc tggctctgca gtcgtccttg ccagggtgcag agggccctga 1300  
caagcctagc gttgtgtcag ggctgaactc gggccctggg catgtgtggg 1350  
gccctctcct gggactactg ctctgcctc ctctgggtgt ggctggaatc 1400  
ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450  
catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500  
ggccctccgg aagggaagg ctacggggca tgtgcctcat cacaccatcc 1550  
atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600  
ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtcctg 1650  
ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700  
tgccacaca gcatgtgcgc tctccctgag tgctgtgta gctggggatg 1750  
gggattccta ggggcagatg aaggacaagc cccactggag tggggttcct 1800  
tgagtggggg aggcaggac gagggaagga aagtaactcc tgactctcca 1850  
ataaaaacct gtccaacctg tgaaa 1875

<210> 285  
<211> 463  
<212> PRT

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;213&gt; Homo Sapien

&lt;400&gt; 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu	1	5	10	15
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp	20	25	30	
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala	35	40	45	
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp	50	55	60	
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val	65	70	75	
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe	80	85	90	
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu	95	100	105	
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys	110	115	120	
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	125	130	135	
Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu	140	145	150	
Gln	Gly	Val	Glu	Glu	Thr	Asn	Ile	Glu	Leu	Leu	Val	Cys	Asn	Tyr	155	160	165	
Glu	Pro	Pro	Gly	Asn	Val	Lys	Gly	Lys	Arg	Pro	Tyr	Gln	Glu	Gly	170	175	180	
Thr	Pro	Cys	Ser	Gln	Cys	Pro	Ser	Gly	Tyr	His	Cys	Lys	Asn	Ser	185	190	195	
Leu	Cys	Glu	Pro	Ile	Gly	Ser	Pro	Glu	Asp	Ala	Gln	Asp	Leu	Pro	200	205	210	
Tyr	Leu	Val	Thr	Glu	Ala	Pro	Ser	Phe	Arg	Ala	Thr	Glu	Ala	Ser	215	220	225	
Asp	Ser	Arg	Lys	Met	Gly	Thr	Pro	Ser	Ser	Leu	Ala	Thr	Gly	Ile	230	235	240	
Pro	Ala	Phe	Leu	Val	Thr	Glu	Val	Ser	Gly	Ser	Leu	Ala	Thr	Lys	245	250	255	
Ala	Leu	Pro	Ala	Val	Glu	Thr	Gln	Ala	Pro	Thr	Ser	Leu	Ala	Thr	260	265	270	
Lys	Asp	Pro	Pro	Ser	Met	Ala	Thr	Glu	Ala	Pro	Pro	Cys	Val	Thr	275	280	285	
Thr	Glu	Val	Pro	Ser	Ile	Leu	Ala	Ala	His	Ser	Leu	Pro	Ser	Leu	290	295	300	

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile	305	310	315
Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser	320	325	330
Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly	335	340	345
Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu	350	355	360
Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro	365	370	375
Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr	380	385	390
Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser	395	400	405
Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser	410	415	420
Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser	425	430	435
Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly	440	445	450
Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe	455	460	

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

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<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

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<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<212> DNA  
<213> Homo Sapien

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ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200  
acaacaatga attggagacc attccaaatc tgggaccagt ctcggaat 250  
attacacttc tctccttggc tggaaacagg attggtgaaa tactccctga 300  
acatctgaaa gagtttcagt cccttgaaac tttggacctt agcagcaaca 350  
atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400  
tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450  
tttggccaac acactccttg tgtaaagct gaacaggaac cgaatctcag 500  
ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550  
aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600  
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gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100  
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atgtctttac aaggcaatgc attttcacaa atgaagaaac tgcaacaatt 1200  
gcattttaat acatcaagcc ttttgtgcga ttgccagcta aaatggctcc 1250  
cacagtgggt ggcggaaaac aactttcaga gctttgtaaa tgccagttgt 1300  
gcccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450  
 gccagcagca gtgattcccc aatgactttt gcttggaata aagacaatga 1500  
 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggccaag 1550  
 gtggcgaggt gatggagtat accaccatcc ttcggctgcg cgagggtggaa 1600  
 tttgccagtg aggggaaata tcagtgtgtc atctccaatc actttggttc 1650  
 atcctactct gtcaaagcca agcttacagt aaatatgctt ccctcattca 1700  
 ccaagacccc catggatctc accatccgag ctggggccat ggcacgcttg 1750  
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 tgggggcaca gacttccag ctgcacggga gagacgcatg catgtgatgc 1850  
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 gtatacagct gcacagctca gaacagtgc ggaagtattt cagcaaatgc 1950  
 aactctgact gtcctagaaa caccatcatt tttgcggcca ctgttgacc 2000  
 gaactgtaac caaggagaa acagccgtcc tacagtgcatt tgctggagga 2050  
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 aaccgagagg cacttttttg cagcaggcaa tcagcttctg attattgtgg 2150  
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 cttggcactg agagaggaaa cgtgcccctc agtgtgatcc cactccaac 2250  
 ctgcgactcc cctcagatga cagccccatc gttagacgat gacggatggg 2300  
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 gttatttgtc atctcaggga acgtagctg acaggcagga tgggtacgtg 2500  
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 aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc tttagatttt 2950

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050  
 ttggacagcc atcagattgt cagccaagag ccttttattt gaaagctcat 3100  
 tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150  
 agattttcag gaagaaaadc acatttgtac ctttaaacag actttagaaa 3200  
 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250  
 tgagaccaaa ggaaaagctt aacatactac ctcaagtga cttttattta 3300  
 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaaagg 3350  
 ataaaaatgc tttattttata cagatgaacc aaaattacaa aaagttatga 3400  
 aaatttttat actgggaatg atgctcatat aagaatacct ttttaacta 3450  
 ttttttaact ttgttttatg caaaaaagta tcttacgtaa attaatgata 3500  
 taaatcatga ttattttatg tattttttata atgccagatt tctttttatg 3550  
 gaaaatgagt tactaaagca ttttaataaa tacctgcctt gtaccatttt 3600  
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 tgtcaatttg aa 3662

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 <212> PRT  
 <213> Homo Sapien

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 Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
 20 25 30  
 Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
 35 40 45  
 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
 50 55 60  
 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
 65 70 75  
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
 80 85 90  
 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
 95 100 105  
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
 110 115 120  
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
 125 130 135

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser	290	295	300
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile	305	310	315
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg	320	325	330
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala	335	340	345
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn	350	355	360
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys	365	370	375
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys	380	385	390
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln	395	400	405
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly	410	415	420
Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp	425	430	435
Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala			

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ile Lys Gly Ser	Asn	Leu Ser Phe Ile	Cys	Ser Ala Ala Ser	Ser
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Ser Asp Ser Pro Met	Thr Phe Ala Trp	Lys Lys Asp Asn	Glu Leu		
	455		460		465
	470		475		480
Leu His Asp Ala	Glu Met Glu Asn Tyr	Ala His Leu Arg Ala	Gln		
	485		490		495
Gly Gly Glu Val	Met Glu Tyr Thr Thr	Ile Leu Arg Leu Arg	Glu		
	500		505		510
Val Glu Phe Ala	Ser Glu Gly Lys Tyr	Gln Cys Val Ile Ser	Asn		
	515		520		525
His Phe Gly Ser	Ser Tyr Ser Val Lys	Ala Lys Leu Thr Val	Asn		
	530		535		540
Met Leu Pro Ser	Phe Thr Lys Thr Pro	Met Asp Leu Thr Ile	Arg		
	545		550		555
Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro		
	560		565		570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro		
	575		580		585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val		
	590		595		600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser		
	605		610		615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr		
	620		625		630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp		
	635		640		645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala		
	650		655		660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser		
	665		670		675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln		
	680		685		690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr		
	695		700		705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val		
	710		715		720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met		
	725		730		735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val		
	740		745		750

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
755 760 765

Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys  
770 775 780

Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
785 790 795

Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
800 805 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
815 820 825

Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
830 835 840

Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
845 850 855

Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
860 865 870

Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
875 880 885

Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
890 895 900

Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
905 910 915

Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
920 925 930

Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
935 940 945

Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
950 955 960

Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
965 970 975

Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
980 985 990

Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
995 1000 1005

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
1010 1015 1020

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
1025 1030 1035

His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
1040 1045 1050

Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 <212> DNA  
 <213> Homo Sapien

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 ttggtgtgtt ctgacataaa taaataatct taaagcagct gttccccctcc 300  
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 agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400  
 gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450  
 ggtgtggtgg tgttttcctt tctttttgaa tttcccacaa gaggagagga 500  
 aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550  
 gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600  
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 ataggtccta ggtttaacag ggccctattt gaccccctgc ttgtggtgct 900  
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 cggaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050  
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350  
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 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800  
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaacaa 2850  
 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900  
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

&lt;211&gt; 640

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 292

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          20          25          30
Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln
          35          40          45
Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
          50          55          60
Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
          65          70          75
Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
          80          85          90
Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
          95          100          105
Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
          110          115          120
Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
          125          130          135
Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
          140          145          150
Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser
          155          160          165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly
          170          175          180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly
          185          190          195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg
          200          205          210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp
          215          220          225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln
          230          235          240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile
          245          250          255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val
          260          265          270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp
          275          280          285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

290	295	300
Asn Pro Trp Asn Cys 305	Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp 310 315	
Ile Lys Asp Met Ala 320	Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys 325 330	
Asn Thr Pro Pro Asn 335	Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp 340 345	
Gln Asn Tyr Phe Thr 350	Cys Tyr Ala Pro Val Ile Val Glu Pro Pro 355 360	
Ala Asp Leu Asn Val 365	Thr Glu Gly Met Ala Ala Glu Leu Lys Cys 370 375	
Arg Ala Ser Thr Ser 380	Leu Thr Ser Val Ser Trp Ile Thr Pro Asn 385 390	
Gly Thr Val Met Thr 395	His Gly Ala Tyr Lys Val Arg Ile Ala Val 400 405	
Leu Ser Asp Gly Thr 410	Leu Asn Phe Thr Asn Val Thr Val Gln Asp 415 420	
Thr Gly Met Tyr Thr 425	Cys Met Val Ser Asn Ser Val Gly Asn Thr 430 435	
Thr Ala Ser Ala Thr 440	Leu Asn Val Thr Ala Ala Thr Thr Thr Pro 445 450	
Phe Ser Tyr Phe Ser 455	Thr Val Thr Val Glu Thr Met Glu Pro Ser 460 465	
Gln Asp Glu Ala Arg 470	Thr Thr Asp Asn Asn Val Gly Pro Thr Pro 475 480	
Val Val Asp Trp Glu 485	Thr Thr Asn Val Thr Thr Ser Leu Thr Pro 490 495	
Gln Ser Thr Arg Ser 500	Thr Glu Lys Thr Phe Thr Ile Pro Val Thr 505 510	
Asp Ile Asn Ser Gly 515	Ile Pro Gly Ile Asp Glu Val Met Lys Thr 520 525	
Thr Lys Ile Ile Ile 530	Gly Cys Phe Val Ala Ile Thr Leu Met Ala 535 540	
Ala Val Met Leu Val 545	Ile Phe Tyr Lys Met Arg Lys Gln His His 550 555	
Arg Gln Asn His His 560	Ala Pro Thr Arg Thr Val Glu Ile Ile Asn 565 570	
Val Asp Asp Glu Ile 575	Thr Gly Asp Thr Pro Met Glu Ser His Leu 580 585	
Pro Met Pro Ala Ile 590	Glu His Glu His Leu Asn His Tyr Asn Ser 595 600	
Tyr Lys Ser Pro Phe Asn His Thr Thr	Thr Val Asn Thr Ile Asn	

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
605 610 615

Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
620 625 630

Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
635 640

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<211> 4053  
<212> DNA

<213> Homo Sapien

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aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150  
gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200  
gcgcccgtcg ggagcttcgg gtagagacct aggccgctgg accgcgatga 250  
gcgcgccgag cctccgtgcg cgcgccgcgg gggtggggct gctgctgtgc 300  
gcggtgctgg ggcgcgctgg ccggtccgac agcggcggtc gcggggaact 350  
cgggcagccc tctggggtag ccgccgagcg cccatgcccc actacctgcc 400  
gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtctt 450  
cccgagccac tcccgtcctg ggtcgtcgg ctggacttaa gtcacaacag 500  
attatctttc atcaaggcaa gttccatgag ccaccttcaa agccttcgag 550  
aagtgaaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600  
gtctcggcaa atattacact tctctccttg gctggaaaca ggattgttga 650  
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ttagcagcaa caatatttca gagctccaaa ctgcatttcc agccctacag 750  
ctcaaatatc tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800  
gtattttgac aatttgcca acacactcct tgtgttaaag ctgaacagga 850  
accgaatctc agctatccca cccaagatgt ttaaactgcc ccaactgcaa 900  
catctcgaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950  
ccaaggcctt ggtgctctga agtctctgaa aatgcaaaga aatggagtaa 1000  
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cagctggacc ataacaacct aacagagatt accaaaggct ggctttacgg 1100  
cttgctgatg ctgcaggaac ttcattctcag ccaaaatgcc atcaacagga 1150  
tcagccctga tgcctgggag ttctgccaga agctcagtga gctggaccta 1200

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350  
aatgaaattt cctggactat tgaagacatg aatggtgctt tctctgggct 1400  
tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450  
ctaaaaaagc cttcactggt ttggatgcat tggagcatct agacctgagt 1500  
gacaacgcaa tcatgtcttt acaaggcaat gcattttcac aaatgaagaa 1550  
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taaaatggct cccacagtgg gtggcgga aaactttca gagctttgta 1650  
aatgccagtt gtgcccattc tcagctgcta aaaggaagaa gcatttttgc 1700  
tgtagccca gatggctttg tgtgtgatga ttttcccaa cccagatca 1750  
cggttcagcc agaaacacag tcggcaataa aaggttcaa tttgagtttc 1800  
atctgctcag ctgccagcag cagtgattcc ccaatgactt ttgcttggaa 1850  
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tccgggcca aggtggcgag gtgatggagt ataccacat cttcggctg 1950  
cgcgaggtgg aatttgccag tgaggggaaa tatcagtgtg tcatctcaa 2000  
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cactgttggga ccgaactgta accaaggag aaacagccgt cctacagtgc 2400  
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cccattggtg gtaaccgaga ggcacttttt tgcagcaggc aatcagcttc 2500  
tgattattgt ggactcagat gtcagtgatg ctgggaaata cacatgtgag 2550  
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atgacggatg ggccactgtg ggtgtcgtga tcatagccgt ggtttgctgt 2700  
gtggtgggca cgtcactcgt gtgggtggtc atcatatacc acacaaggcg 2750  
gaggaatgaa gattgcagca ttaccaacac agatgagacc aacttgccag 2800

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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ttcagggtgct ggatttttct taccacaaca tgacagtagt gggacctgcc 2950  
atattgacaa tagcagtga gctgatgtgg aagctgccac agatctgttc 3000  
ctttgtccgt ttttgggatc cacaggccct atgtatttga agggaaatgt 3050  
gtatggctca gatccttttg aaacatatca tacaggttgc agtcctgacc 3100  
caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150  
gagtgtacc catgtttctca tccttcagaa gaatcctgcg aacggagctt 3200  
cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250  
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<210> 294  
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<212> PRT  
<213> Homo Sapien

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Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg
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Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys
				50					55					60
Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp
				65					70					75
Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				80					85					90
Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu
				95					100					105
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser
				110					115					120
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu
				125					130					135
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu
				140					145					150
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro
				155					160					165
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr
				170					175					180
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu
				185					190					195
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys
				200					205					210
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn
				215					220					225
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala
				230					235					240
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met
				245					250					255
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu
				260					265					270
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly
				275					280					285
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn
				290					295					300
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu
				305					310					315
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser
				320					325					330
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser	335	340	345
				350					355					360			
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile	365	370	375
				380					385					390			
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg			
				395					400					405			
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala			
				410					415					420			
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn			
				425					430					435			
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys			
				440					445					450			
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys			
				455					460					465			
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln			
				470					475					480			
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly			
				485					490					495			
Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp			
				500					505					510			
Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala			
				515					520					525			
Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser			
				530					535					540			
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu			
				545					550					555			
Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln			
				560					565					570			
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu			
				575					580					585			
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn			
				590					595					600			
His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn			
				605					610					615			
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg			
				620					625					630			
Ala	Gly	Ala	Met	Ala	Arg	Leu	Glu	Cys	Ala	Ala	Val	Gly	His	Pro			
				635					640					645			
Ala	Pro	Gln	Ile	Ala	Trp	Gln	Lys	Asp	Gly	Gly	Thr	Asp	Phe	Pro			
				645					650					655			
Ala	Ala	Arg	Glu	Arg	Arg	Met	His	Val	Met	Pro	Glu	Asp	Asp	Val			

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Phe	Phe	Ile	Val	Asp	Val	Lys	Ile	Glu	Asp	Ile	Gly	Val	Tyr	Ser
				665					670					675
Cys	Thr	Ala	Gln	Asn	Ser	Ala	Gly	Ser	Ile	Ser	Ala	Asn	Ala	Thr
				680					685					690
Leu	Thr	Val	Leu	Glu	Thr	Pro	Ser	Phe	Leu	Arg	Pro	Leu	Leu	Asp
				695					700					705
Arg	Thr	Val	Thr	Lys	Gly	Glu	Thr	Ala	Val	Leu	Gln	Cys	Ile	Ala
				710					715					720
Gly	Gly	Ser	Pro	Pro	Pro	Lys	Leu	Asn	Trp	Thr	Lys	Asp	Asp	Ser
				725					730					735
Pro	Leu	Val	Val	Thr	Glu	Arg	His	Phe	Phe	Ala	Ala	Gly	Asn	Gln
				740					745					750
Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr
				755					760					765
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val
				770					775					780
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met
				785					790					795
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val
				800					805					810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val
				815					820					825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys
				830					835					840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro
				845					850					855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly
				860					865					870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser
				875					880					885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr
				890					895					900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr
				905					910					915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr
				920					925					930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His
				935					940					945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr
				950					955					960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

965 970 975

Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
980 985 990

Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
995 1000 1005

Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
1010 1015 1020

Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
1025 1030 1035

Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
1040 1045 1050

Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
1055 1060 1065

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
1070 1075 1080

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
1085 1090 1095

His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
1100 1105 1110

Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
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<211> 18

<212> DNA

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<400> 295

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<210> 296

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 296

cctaaactga actggacca 19

<210> 297

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 297

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
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<210> 298

<211> 24

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 298

acagctgcac agctcagaac agtg 24

<210> 299

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 299

cattcccagt ataaaaattt tc 22

<210> 300

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 300

gggtcttggt gaatgagg 18

<210> 301

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 301

gtgcctctcg gttaccacca atgg 24

<210> 302

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 302

gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

<210> 303

<211> 28

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Synthetic oligonucleotide Probe

<400> 303

gcctttgaca accttcagtc actagtgg 28

<210> 304

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide Probe

<400> 304

ccccatgtgt ccatgactgt tccc 24

<210> 305

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide Probe

<400> 305

tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide Probe

<400> 306

actccaagga aatcgatcc gtgc 24

<210> 307

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

ttagcagctg aggatgggca caac 24

<210> 308

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide Probe

<400> 308

actccaagga aatcgatcc gtgc 24

<210> 309

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 50

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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<211> 3003

<212> DNA

<213> Homo Sapien

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<211> 509

<212> PRT

<213> Homo Sapien



## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 35      40      45
Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
 50      55      60
Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
 65      70      75
Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
 80      85      90
Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
 95      100      105
Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
110      115      120
Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
125      130      135
Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
140      145      150
Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
155      160      165
Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
170      175      180
Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
185      190      195
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200      205      210
Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
215      220      225
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245      250      255
Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
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Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
275      280      285
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Thr Asp Pro Gln	Lys Pro Arg Gly Asp	Val Phe Ser Val Leu	Val
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His Ser Cys Asn	Phe Asp His Gly Leu	Cys Gly Trp Ile Arg	Glu
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Lys Asp Asn Asp	Leu His Trp Glu Pro	Ile Arg Asp Pro Ala	Gly
	410	415	420
Gly Gln Tyr Leu	Thr Val Ser Ala Ala	Lys Ala Pro Gly Gly	Lys
	425	430	435
Ala Ala Arg Leu	Val Leu Pro Leu Gly	Arg Leu Met His Ser	Gly
	440	445	450
Asp Leu Cys Leu	Ser Phe Arg His Lys	Val Thr Gly Leu His	Ser
	455	460	465
Gly Thr Leu Gln	Val Phe Val Arg Lys	His Gly Ala His Gly	Ala
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Ala Leu Trp Gly	Arg Asn Gly Gly His	Gly Trp Arg Gln Thr	Gln
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<400> 316

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgcacttgt aggaccacg tacg 24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<210> 320  
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35 40 45  
His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg  
50 55 60  
Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser  
65 70 75  
Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Lys Pro Val Val	Gln 140	Ile His Pro Pro	Ser 145	Gly Ala Val Glu	Tyr 150
Val Gly Asn Met	Thr 155	Leu Thr Cys His	Val 160	Glu Gly Gly Thr	Arg 165
Leu Ala Tyr Gln	Trp 170	Leu Lys Asn Gly	Arg 175	Pro Val His Thr	Ser 180
Ser Thr Tyr Ser	Phe 185	Ser Pro Gln Asn	Asn 190	Thr Leu His Ile	Ala 195
Pro Val Thr Lys	Glu 200	Asp Ile Gly Asn	Tyr 205	Ser Cys Leu Val	Arg 210
Asn Pro Val Ser	Glu 215	Met Glu Ser Asp	Ile 220	Ile Met Pro Ile	Ile 225
Tyr Tyr Gly Pro	Tyr 230	Gly Leu Gln Val	Asn 235	Ser Asp Lys Gly	Leu 240
Lys Val Gly Glu	Val 245	Phe Thr Val Asp	Leu 250	Gly Glu Ala Ile	Leu 255
Phe Asp Cys Ser	Ala 260	Asp Ser His Pro	Pro 265	Asn Thr Tyr Ser	Trp 270
Ile Arg Arg Thr	Asp 275	Asn Thr Thr Tyr	Ile 280	Ile Lys His Gly	Pro 285
Arg Leu Glu Val	Ala 290	Ser Glu Lys Val	Ala 295	Gln Lys Thr Met	Asp 300
Tyr Val Cys Cys	Ala 305	Tyr Asn Asn Ile	Thr 310	Gly Arg Gln Asp	Glu 315
Thr His Phe Thr	Val 320	Ile Ile Thr Ser	Val 325	Gly Leu Glu Lys	Leu 330
Ala Gln Lys Gly	Lys 335	Ser Leu Ser Pro	Leu 340	Ala Ser Ile Thr	Gly 345
Ile Ser Leu Phe	Leu 350	Ile Ile Ser Met	Cys 355	Leu Leu Phe Leu	Trp 360
Lys Lys Tyr Gln	Pro 365	Tyr Lys Val Ile	Lys 370	Gln Lys Leu Glu	Gly 375
Arg Pro Glu Thr	Glu 380	Tyr Arg Lys Ala	Gln 385	Thr Phe Ser Gly	His 390
Glu Asp Ala Leu	Asp 395	Asp Phe Gly Ile	Tyr 400	Glu Phe Val Ala	Phe 405

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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410	420
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<210> 321  
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<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 323  
 ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397  
 <212> DNA  
 <213> Homo Sapien

<400> 324  
 gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50  
 cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100  
 acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150  
 tggatgatag aatttttatgc cccgtggtgc cctgcttgtc aaaatcttca 200  
 accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250  
 ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatc 300

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

ataactgctc ttctactat ttatcattgt aaagatggtg aatttaggcg 350  
ctatcagggg ccaaggacta agaaggactt cataaacttt ataagtata 400  
aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450  
gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500  
gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550  
catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600  
ctctgtatga tatttggtggc agattgcctt tgtccttcaa aaaggcgag 650  
accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700  
aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750  
tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800  
gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850  
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acataaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050  
gatggtttta atagttctct aatttttgaa aaatcgtgcc aagcaataag 1100  
atztatgtat atttgtttta taataacctt tttcaagtct gagttttgaa 1150  
aatttacatt tcccaagtat tgcattattg aggtatttaa gaagattatt 1200  
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agaaatgtgt atttcagtga caatttcgtg gtcttttttag aggtatattc 1350  
caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400  
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tgaagtgaa cattcctgat ttttgtctga tgtgaaaaag ctttggtatt 1800  
ttacattttg aaaattcaaa gaagcttaat ataaaagttt gcattctact 1850  
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## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

atacagaaaag	tctttaattg	attttacagt	ctgtaatgct	tgatgtttta	1950
aaataataac	atttttatat	tttttaaaag	acaaacttca	tattatcctg	2000
tgttctttcc	tgactggtaa	tattgtgtgg	gatttcacag	gtaaaagtca	2050
gtaggatgga	acatttttagt	gtattttttac	tccttaaaga	gctagaatac	2100
atagttttca	ccttaaaaga	agggggaaaa	tcataaatac	aatgaatcaa	2150
ctgaccatta	cgtagtagac	aatttctgta	atgtcccctt	ctttctaggc	2200
tctgttgctg	tgtgaatcca	ttagattttac	agtatcgtaa	tatacaagtt	2250
ttcttttaaag	ccctctcctt	tagaatttaa	aatattgtac	cattaaagag	2300
tttggatgtg	taacttgtga	tgcccttagaa	aaatatccta	agcacaaaat	2350
aaacctttct	aaccacttca	ttaaagctga	aaaaaaaaaa	aaaaaaa	2397

**<210> 325**

**<211> 280**

<212> PRT

<213> Homo Sapien

**<400> 325**

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Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn  
20 25 30

Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly  
35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln  
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp  
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly  
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His  
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys  
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile  
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser  
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys  
155 160

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser  
170 175 180



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu  
185 190 195  
Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys  
200 205 210  
Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu  
215 220 225  
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu  
230 235 240  
Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu  
245 250 255  
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser  
260 265 270  
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser  
275 280

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

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<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttccccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgcggag acccgtgata attcggtaac taattcaaca 50  
aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100  
ggacaggcgg attggaagag cgggaaggct ctggcccaga gcagtgtgac 150  
acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200  
ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250  
cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300  
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ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400  
tacctggctc accctgtgaa tgcctacaaa ctggtgaagc ggctaaacac 450  
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ggaccagggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650  
caatgctgag tgtggatgac tgctttggga tgggccgctc ggcctacaat 700  
gaaggggact attatcatac ggtgtttgtg atggagcagg tgctaaagca 750  
gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800  
acctcagcta tgctgtcttc cagttgggtg atctgcaccg tgccctggag 850  
ctcaccgcc gcctgtctc ccttgacca agccacgaac gagctggagg 900  
gaatctgcgg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950  
taacaaatca gacagaagct gagctagcaa cccagaagg catctatgag 1000  
aggcctgtgg actacctgcc tgagagggat gtttacgaga gcctctgtcg 1050

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 ggtaccacca tggcaacagg gccccacagc tgctcattgc ccccttcaaa 1150  
 gaggaggacg agtgggacag cccgcacatc gtcagggtact acgatgtcat 1200  
 gtctgatgag gaaatcgaga ggatcaagga gatcgcaaaa cctaaacttg 1250  
 cacgagccac cgttcgtgat cccaagacag gagtcctcac tgtcgccagc 1300  
 taccgggttt ccaaaagctc ctggctagag gaagatgatg accctgttgt 1350  
 ggcccgagta aatcgtcgga tgcagcatat cacagggtta acagtaaaga 1400  
 ctgcagaatt gttacagggt gcaaattatg gagtgggagg acagtatgaa 1450  
 ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaacaga 1500  
 ggggaatagg ttagcgacgt ttcttaacta catgagtcat gtagaagctg 1550  
 gtggtgccac cgtcttcctt gatctggggg ctgcaatttg gcctaagaag 1600  
 ggtacagctg tgttctggta caacctcttg cggagcgggg aagggtgacta 1650  
 ccgaacaaga catgctgcct gccctgtgct tgtgggctgc aagtgggtct 1700  
 ccaataagtg gttccatgaa cgaggacagg agttcttgag accttggtga 1750  
 tcaacagaag ttgactgaca tccttttctg tccttcccct tcctggtcct 1800  
 tcagcccatg tcaacgtgac agacacctt gtatgttctt ttgtatgttc 1850  
 ctatcaggct gatTTTTGGA gaaatgaatg tttgtctgga gcagagggag 1900  
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 gttagctgtc tagcgcttag caagggtcct ttgtacctca ggtgttttag 2050  
 gtgtgagatg tttcagtga ccaaagttct gataccttgt ttacatgttt 2100  
 gtttttatgg catttctatc tattgtggct ttacaaaaa ataaaatgtc 2150  
 cctaccagaa aaaaaaaaa 2168

<210> 332  
 <211> 533  
 <212> PRT  
 <213> Homo Sapien

<400> 332  
 Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val  
 1 5 10 15  
 Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met  
 20 25 30  
 Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys  
 35 40 45  
 Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser  
 50 55 60

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp	65	70	75
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val	80	85	90
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu	95	100	105
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg	110	115	120
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala	125	130	135
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile	140	145	150
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser	155	160	165
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly	170	175	180
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln	185	190	195
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu	200	205	210
Asp	Tyr	Leu	Ser	Tyr	Ala	Val	Phe	Gln	Leu	Gly	Asp	Leu	His	Arg	215	220	225
Ala	Leu	Glu	Leu	Thr	Arg	Arg	Leu	Leu	Ser	Leu	Asp	Pro	Ser	His	230	235	240
Glu	Arg	Ala	Gly	Gly	Asn	Leu	Arg	Tyr	Phe	Glu	Gln	Leu	Leu	Glu	245	250	255
Glu	Glu	Arg	Glu	Lys	Thr	Leu	Thr	Asn	Gln	Thr	Glu	Ala	Glu	Leu	260	265	270
Ala	Thr	Pro	Glu	Gly	Ile	Tyr	Glu	Arg	Pro	Val	Asp	Tyr	Leu	Pro	275	280	285
Glu	Arg	Asp	Val	Tyr	Glu	Ser	Leu	Cys	Arg	Gly	Glu	Gly	Val	Lys	290	295	300
Leu	Thr	Pro	Arg	Arg	Gln	Lys	Arg	Leu	Phe	Cys	Arg	Tyr	His	His	305	310	315
Gly	Asn	Arg	Ala	Pro	Gln	Leu	Leu	Ile	Ala	Pro	Phe	Lys	Glu	Glu	320	325	330
Asp	Glu	Trp	Asp	Ser	Pro	His	Ile	Val	Arg	Tyr	Tyr	Asp	Val	Met	335	340	345
Ser	Asp	Glu	Glu	Ile	Glu	Arg	Ile	Lys	Glu	Ile	Ala	Lys	Pro	Lys	350	355	360
Leu	Ala	Arg	Ala	Thr	Val	Arg	Asp	Pro	Lys	Thr	Gly	Val	Leu	Thr	365	370	375

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val	Ala	Ser	Tyr	Arg	Val	Ser	Lys	Ser	Ser	Trp	Leu	Glu	Glu	Asp
				380					385					390
Asp	Asp	Pro	Val	Val	Ala	Arg	Val	Asn	Arg	Arg	Met	Gln	His	Ile
				395					400					405
Thr	Gly	Leu	Thr	Val	Lys	Thr	Ala	Glu	Leu	Leu	Gln	Val	Ala	Asn
				410					415					420
Tyr	Gly	Val	Gly	Gly	Gln	Tyr	Glu	Pro	His	Phe	Asp	Phe	Ser	Arg
				425					430					435
Arg	Pro	Phe	Asp	Ser	Gly	Leu	Lys	Thr	Glu	Gly	Asn	Arg	Leu	Ala
				440					445					450
Thr	Phe	Leu	Asn	Tyr	Met	Ser	Asp	Val	Glu	Ala	Gly	Gly	Ala	Thr
				455					460					465
Val	Phe	Pro	Asp	Leu	Gly	Ala	Ala	Ile	Trp	Pro	Lys	Lys	Gly	Thr
				470					475					480
Ala	Val	Phe	Trp	Tyr	Asn	Leu	Leu	Arg	Ser	Gly	Glu	Gly	Asp	Tyr
				485					490					495
Arg	Thr	Arg	His	Ala	Ala	Cys	Pro	Val	Leu	Val	Gly	Cys	Lys	Trp
				500					505					510
Val	Ser	Asn	Lys	Trp	Phe	His	Glu	Arg	Gly	Gln	Glu	Phe	Leu	Arg
				515					520					525
Pro	Cys	Gly	Ser	Thr	Glu	Val	Asp							
				530										

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 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 333  
 ccaggcacaa tttccaga 18

<210> 334  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 334  
 ggacccttct gtgtgccag 19

<210> 335  
 <211> 19  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 335  
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<210> 336  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 336  
 acactcagca ttgcctggta cttg 24

<210> 337  
 <211> 45  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 337  
 gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338  
 <211> 2789

<212> DNA  
 <213> Homo Sapien

<400> 338  
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 cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350  
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 gtgcagcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450  
 atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500  
 tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550  
 cccctactac agggacccca acaagcccta caagaagggtg ctcaggactc 600  
 ggtacatcca gacagagctg ggctcccgtg agcggttgct ggtggctgtc 650  
 ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700  
 ggtggcccat cacttccctc gggttactcta cttcactggg cagcgggggg 750

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 cgactacgac tggttcttca tcatgcagga tgacacatat gtgcaggccc 900  
 cccgcctggc agcccttgct ggccacctca gcatcaacca agacctgtac 950  
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 gagtggcttg gacgctgcct cattgactct ctgggcgtcg gctgtgtctc 1150  
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 accctgagaa ggaagggagc tcggctttcc tgagtgcctt cgccgtgcac 1250  
 cctgtctccg aaggtaccct catgtaccgg ctccacaaac gcttcagcgc 1300  
 tctggagttg gagcgggctt acagtgaat agaacaactg caggctcaga 1350  
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 cccgttgggc tccctgctcc ttccacacca cactctcgtt ttgaggtgct 1450  
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 ctcccaagtg cccactacag ggggctagca gggcgacgt gggatgatgcg 1550  
 ttggagactg ccctggagca gctcaatcgg cgctatcagc cccgcctgcg 1600  
 cttccagaag cagcgactgc tcaacggcta tcggcgcttc gaccagcac 1650  
 ggggcatgga gtacaccctg gacctgctgt tggaatgtgt gacacagcgt 1700  
 gggcaccggc gggccctggc tcgcagggc agcctgctgc ggccactgag 1750  
 ccgggtggaa atcctaccta tgccctatgt cactgaggcc acccgagtgc 1800  
 agctggtgct gccactcctg gtggctgaag ctgctgcagc cccggctttc 1850  
 ctcgaggcgt ttgcagccaa tgtcctggag ccacgagaac atgcattgct 1900  
 caccctgttg ctggtctacg ggccacgaga aggtggccgt ggagctccag 1950  
 acccatttct tggggtgaag gctgcagcag cggagttaga gcgacggtac 2000  
 cctgggacga ggctggcctg gctcgtctg cgagcagagg ccccttcca 2050  
 ggtgcgactc atggacgtgg tctcgaagaa gcaccctgtg gacactctct 2100  
 tcttccttac caccgtgtgg acaaggcctg ggcccgaagt cctcaaccgc 2150  
 tgtcgcata atgccatctc tggctggcag gccttctttc cagtccattt 2200  
 ccaggagttc aatcctgccc tgtcaccaca gagatcacc ccaggggccc 2250  
 cgggggctgg ccctgacccc ccctcccctc ctggtgctga cccctcccgg 2300  
 ggggctccta taggggggag atttgaccgg caggcttctg cggagggtg 2350

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 tggcaggcca ggaagaggag gaagccctgg aggggctgga ggtgatggat 2450  
 gttttcctcc ggttctcagg gctccacctc tttcgggccg tagagccagg 2500  
 gctggtgcag aagttctccc tgcgagactg cagcccacgg ctgagtgaag 2550  
 aactctacca ccgctgccgc ctgagcaacc tggaggggct agggggccgt 2600  
 gcccagctgg ctatggctct ctttgagcag gagcaggcca atagcactta 2650  
 gccgcctgg gggccctaac ctctattacct ttcctttgtc tgcctcagcc 2700  
 ccaggaaggg caaggcaaga tggtagacag atagagaatt gttgctgtat 2750  
 tttttaaata tgaaaatgtt attaaacatg tcttctgcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
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Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
			20						25					30
Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
			35						40					45
Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
			50						55					60
Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
			65						70					75
Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
			80						85					90
Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
			95						100					105
Val	Leu	Thr	Ser	Arg	Ala	Thr	Leu	Ser	Thr	Leu	Ala	Val	Ala	Val
			110						115					120
Asn	Arg	Thr	Val	Ala	His	His	Phe	Pro	Arg	Leu	Leu	Tyr	Phe	Thr
			125						130					135
Gly	Gln	Arg	Gly	Ala	Arg	Ala	Pro	Ala	Gly	Met	Gln	Val	Val	Ser
			140						145					150
His	Gly	Asp	Glu	Arg	Pro	Ala	Trp	Leu	Met	Ser	Glu	Thr	Leu	Arg
			155						160					165
His	Leu	His	Thr	His	Phe	Gly	Ala	Asp	Tyr	Asp	Trp	Phe	Phe	Ile
			170						175					180
Met	Gln	Asp	Asp	Thr	Tyr	Val	Gln	Ala	Pro	Arg	Leu	Ala	Ala	Leu
			185						190					195



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Gly His Leu	Ser 200	Ile Asn Gln Asp	Leu 205	Tyr Leu Gly Arg	Ala 210
Glu Glu Phe Ile	Gly 215	Ala Gly Glu Gln	Ala 220	Arg Tyr Cys His	Gly 225
Gly Phe Gly Tyr	Leu 230	Leu Ser Arg Ser	Leu 235	Leu Leu Arg Leu	Arg 240
Pro His Leu Asp	Gly 245	Cys Arg Gly Asp	Ile 250	Leu Ser Ala Arg	Pro 255
Asp Glu Trp Leu	Gly 260	Arg Cys Leu Ile	Asp 265	Ser Leu Gly Val	Gly 270
Cys Val Ser Gln	His 275	Gln Gly Gln Gln	Tyr 280	Arg Ser Phe Glu	Leu 285
Ala Lys Asn Arg	Asp 290	Pro Glu Lys Glu	Gly 295	Ser Ser Ala Phe	Leu 300
Ser Ala Phe Ala	Val 305	His Pro Val Ser	Glu 310	Gly Thr Leu Met	Tyr 315
Arg Leu His Lys	Arg 320	Phe Ser Ala Leu	Glu 325	Leu Glu Arg Ala	Tyr 330
Ser Glu Ile Glu	Gln 335	Leu Gln Ala Gln	Ile 340	Arg Asn Leu Thr	Val 345
Leu Thr Pro Glu	Gly 350	Glu Ala Gly Leu	Ser 355	Trp Pro Val Gly	Leu 360
Pro Ala Pro Phe	Thr 365	Pro His Ser Arg	Phe 370	Glu Val Leu Gly	Trp 375
Asp Tyr Phe Thr	Glu 380	Gln His Thr Phe	Ser 385	Cys Ala Asp Gly	Ala 390
Pro Lys Cys Pro	Leu 395	Gln Gly Ala Ser	Arg 400	Ala Asp Val Gly	Asp 405
Ala Leu Glu Thr	Ala 410	Leu Glu Gln Leu	Asn 415	Arg Arg Tyr Gln	Pro 420
Arg Leu Arg Phe	Gln 425	Lys Gln Arg Leu	Leu 430	Asn Gly Tyr Arg	Arg 435
Phe Asp Pro Ala	Arg 440	Gly Met Glu Tyr	Thr 445	Leu Asp Leu Leu	Leu 450
Glu Cys Val Thr	Gln 455	Arg Gly His Arg	Arg 460	Ala Leu Ala Arg	Arg 465
Val Ser Leu Leu	Arg 470	Pro Leu Ser Arg	Val 475	Glu Ile Leu Pro	Met 480
Pro Tyr Val Thr	Glu 485	Ala Thr Arg Val	Gln 490	Leu Val Leu Pro	Leu 495
Leu Val Ala Glu	Ala 500	Ala Ala Ala Pro	Ala 505	Phe Leu Glu Ala	Phe 510

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Ala Asn Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu
	515					520					525
Leu Leu Val Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp
	530					535					540
Pro Phe Leu Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg
	545					550					555
Tyr Pro Gly Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala
	560					565					570
Pro Ser Gln Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro
	575					580					585
Val Asp Thr Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly
	590					595					600
Pro Glu Val Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp
	605					610					615
Gln Ala Phe Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu
	620					625					630
Ser Pro Gln Arg	Ser	Pro	Pro	Gly	Pro	Pro	Gly	Ala	Gly	Pro	Asp
	635					640					645
Pro Pro Ser Pro	Pro	Gly	Ala	Asp	Pro	Ser	Arg	Gly	Ala	Pro	Ile
	650					655					660
Gly Gly Arg Phe	Asp	Arg	Gln	Ala	Ser	Ala	Glu	Gly	Cys	Phe	Tyr
	665					670					675
Asn Ala Asp Tyr	Leu	Ala	Ala	Arg	Ala	Arg	Leu	Ala	Gly	Glu	Leu
	680					685					690
Ala Gly Gln Glu	Glu	Glu	Glu	Ala	Leu	Glu	Gly	Leu	Glu	Val	Met
	695					700					705
Asp Val Phe Leu	Arg	Phe	Ser	Gly	Leu	His	Leu	Phe	Arg	Ala	Val
	710					715					720
Glu Pro Gly Leu	Val	Gln	Lys	Phe	Ser	Leu	Arg	Asp	Cys	Ser	Pro
	725					730					735
Arg Leu Ser Glu	Glu	Leu	Tyr	His	Arg	Cys	Arg	Leu	Ser	Asn	Leu
	740					745					750
Glu Gly Leu Gly	Gly	Arg	Ala	Gln	Leu	Ala	Met	Ala	Leu	Phe	Glu
	755					760					765
Gln Glu Gln Ala	Asn	Ser	Thr								
	770										

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

cgagtggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50

## CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tgcccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100  
ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150  
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350  
accaaact gtgacaaagc agagtcttc agttctgaaa atgttaaagt 400  
gtttgagtca attaatatgg acacaaatga catgtggtta atgatgagaa 450  
aagcttaca atacgccttt gataagtata gagaccaata caactgggtc 500  
ttccttgac gccccactac gtttgctatc attgaaaacc taaagtattt 550  
tttgtaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600  
aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700  
tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800  
gatggaaaag atgtatttaa taccaaactc gttgggcttt ctattaaaga 850  
ggcaatgact tatcaccca accaggtagt agaaggctgt tgttcagata 900  
tggtgtttac ttttaattga ctgactccaa atcagatgca tgtgatgatg 950  
tatggggat accgccttag ggcatttggg catattttca atgatgcatt 1000  
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agcgtgaata tgatctttgt ataggacgtg tgttgtcatt atttgtagta 1100  
gtaactacat atccaatata gctgtatgtt tctttttctt ttctaatttg 1150  
gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaata 1200  
gggtggtttt tttctttaaa acacatgaac attgtaaatg tgttggaaag 1250  
aagtgtttta agaataataa ttttgcaaat aaactattaa taaatattat 1300  
atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350  
tttctgatt gggttaaaaa ttttaacagg tcttttagcgt tctaagatat 1400  
gcaaatgata tctctagtgt tgaatttgtg attaaagtaa aacttttagc 1450  
tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctcccaa 1500  
gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550  
attaaagtga aagttgaaaa at 1572

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 318

<212> PRT

<213> Homo Sapien

<400> 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly	1	5	10	15
Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile	20	25	30	
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	35	40	45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg	50	55	60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val	65	70	75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	80	85	90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val	95	100	105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	110	115	120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp	125	130	135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile	140	145	150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln	155	160	165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr	170	175	180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys	185	190	195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln	200	205	210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val	215	220	225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala	230	235	240	
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile	245	250	255	
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys	260	265	270	
Cys	Ser	Asp	Met	Ala	Val	Thr	Phe	Asn	Gly	Leu	Thr	Pro	Asn	Gln	275	280	285	
Met	His	Val	Met	Met	Tyr	Gly	Val	Tyr	Arg	Leu	Arg	Ala	Phe	Gly				

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

290

295

300

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser  
305 310 315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaagtc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tgggtgtctca tgggg 25

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 347  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 347  
ccctcatgta ccggctcc 18  
  
<210> 348  
<211> 48  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 348  
ggattctaatt acgactcact atagggctca gaaaagcgca acagagaa 48  
  
<210> 349  
<211> 47  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 349  
ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47  
  
<210> 350  
<211> 48  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 350  
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<211> 48  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 351  
ctatgaaatt aaccctcact aaagggacga ggaagatggg cggatggt 48  
  
<210> 352  
<211> 47  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 352  
ggattctaatacgcactcactatagggcaccacgcgtccggctgctt 47

<210> 353  
<211> 48  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 353  
ctatgaaattaacccctcactaaagggacggggacaccacggaccaga 48

<210> 354  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 354  
ggattctaatacgcactcactatagggcttgctgcggtttttgttcctg 48

<210> 355  
<211> 48  
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<220>  
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<400> 355  
ctatgaaattaacccctcactaaagggagctgccgatcccactggtatt 48

<210> 356  
<211> 46  
<212> DNA  
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<220>  
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<400> 356  
ggattctaatacgcactcactatagggcggaacctggccggcctctg 46

<210> 357  
<211> 48  
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<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 357  
ctatgaaattaacccctcactaaagggagcccgggcatggtctcagtta 48

<210> 358  
<211> 47  
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<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Synthetic Oligonucleotide Probe

<400> 358

ggattctaatacgcactcact atagggcggaagatggcga ggaggag 47

<210> 359

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 359

ctatgaaatt aaccctcact aaaggacacaggccacaaa cggaatc 48

<210> 360

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 360

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<210> 361

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 361

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<210> 362

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 362

ggattctaatacgcactcact atagggcccg cctcgctcct gtcctg 47

<210> 363

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 363

ctatgaaatt aaccctcact aaaggaggga ttgccgcgac cctcacag 48

<210> 364

<211> 47



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 364  
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<210> 365  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 365  
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<210> 366  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 366  
 ggattctaatacgcactcactatagggcgcgatggcagcgatgagg 48

<210> 367  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 367  
 ctatgaaattaacccctcactaaagggacagacggggcagagggagtg 47

<210> 368  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 368  
 ggattctaatacgcactcactatagggccagaggcgtagagagaaac 47

<210> 369  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 369

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt  
ctatgaaatt aaccctcact aaagggaaag acatgtcatc gggagtgg 48

<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

ggattctaatt acgactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggattctaatt acgactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

ggattctaatt acgactcact atagggccag ctacccgcag gaggagg 47

<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaaatt aaccctcact aaagggatcc caggatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

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 agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100  
 aaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150  
 tgcttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200  
 atttctcagt gcctgtttca tcaccagatg tggtgtgaca tttcgcatct 250  
 ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300  
 ctctcctgct acaattatgg atcagggtca gtcaagaatt gttgtccatt 350  
 gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400  
 tttcctgggc gttaagtta aagaactgct cagccatggg ggctcacctg 450  
 gtggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500  
 taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgaggggtc 550  
 agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600  
 gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650  
 gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700  
 tcaattatct tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750  
 ggaaaatctc ttttaagaaca gaaggcaca ctcaaattgtg taaagaagga 800  
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850  
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

Met Asn Ser Ser Lys Ser Ser Glu Thr Gln Cys Thr Glu Arg Gly  
 1 5 10 15

Cys Phe Ser Ser Gln Met Phe Leu Trp Thr Val Ala Gly Ile Pro  
 20 25 30

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr
      35                                40                                45

Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro
      50                                55                                60

Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
      65                                70                                75

Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser
      80                                85                                90

Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu
      95                                100                               105

Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser
     110                               115                               120

Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg
     125                               130                               135

Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp
     140                               145                               150

Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp
     155                               160                               165

Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala
     170                               175                               180

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
     185                               190                               195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
     200                               205                               210

Asn Pro Leu Asn Lys Gly Lys Ser Leu
     215

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<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

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<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

ggccttgag acaaccgt 18

<210> 383

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 383

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<210> 384

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 384

cagctgccct tccccaacca 20

<210> 385

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 385

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 386  
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<210> 387  
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<223> synthetic oligonucleotide probe  
  
<400> 387  
gggcatcac agctccct 18

<210> 388  
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<210> 389  
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<400> 389  
tgccagctgc atgctgccag tt 22

<210> 390  
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<210> 391  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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atgtcctcca tgcccacgcg 20

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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<210> 396

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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gaagagcaca gctgcagatc c 21

<210> 397

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<220>

<223> synthetic oligonucleotide probe

<400> 397

gaggtgtcct ggctttgta gt 22

<210> 398

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide probe

<400> 398

cctctggcgc cccactcaa 20

<210> 399

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> synthetic oligonucleotide probe

<400> 399

ccaggagagc tggcgatg 18

<210> 400

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<400> 400

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<210> 401

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide probe

<400> 401

cacagagcat ttgtccatca gcagttcag 29

<210> 402

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<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide probe

<400> 402

ggcagagact tccagtcact ga 22



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 403  
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<210> 404  
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<400> 404  
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<210> 405  
<211> 23  
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<223> Synthetic oligonucleotide probe  
  
<400> 405  
gggacgtgct tctacaagaa cag 23  
  
<210> 406  
<211> 26  
<212> DNA  
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<223> Synthetic oligonucleotide probe  
  
<400> 406  
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<210> 407  
<211> 31  
<212> DNA  
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<400> 407  
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<210> 408  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 408  
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<210> 409  
<211> 23  
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<220>  
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<400> 409  
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<210> 410  
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<400> 410  
gccaggcctc acattcgt 18

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<220>  
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<400> 411  
ctccctgaat ggcagcctga gca 23

<210> 412  
<211> 24  
  
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<400> 412  
aggtgtttat taagggccta cgct 24

<210> 413  
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<212> DNA  
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<220>  
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<400> 413  
cagagcagag ggtgccttg 19

<210> 414  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>  
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<210> 415  
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<220>  
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<400> 415  
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<210> 416  
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<213> Artificial Sequence

<220>  
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<400> 416  
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<210> 417  
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<220>  
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<210> 418  
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<220>  
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<400> 418  
gggactgaac tgccagcttc 20

<210> 419  
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<220>  
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gggccctaac ctcattacct tt 22

<210> 420

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 23  
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<220>  
<223> synthetic oligonucleotide probe

<400> 420  
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<210> 421  
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<212> DNA  
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<220>  
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<400> 421  
tctgtccacc atcttgccctt g 21

<210> 422  
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<212> DNA  
<213> Homo Sapien

<400> 422  
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atggcgctga ggcgccacc gcgactccgg ctctgcgctc ggctgcctga 100  
cttcttctctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150  
tcaaattccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200  
ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250  
gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300  
ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350  
aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400  
cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450  
ctgtgcaagt gaagccagt acccctgtct gtagagtgcc gaaggctgta 500  
ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550  
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acaggcactt tgggtgtcac tgctgttcac aaggacgact ctgggcagta 700  
ctactgcatt gcttccaatg acgcaggctc agccagggtg gaggagcagg 750  
agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800  
gttgctcctg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850  
cagacgtggc tacttcatca acaataaaca ggatggagaa agttacaaga 900

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

acccagggaa accagatgga gttaactaca tccgcactga cgaggagggc 950  
 gacttcagac acaagtcacg gtttgtgatc tgagacccgc ggtgtggctg 1000  
 agagcgcaca gagcgcacgt gcacatacct ctgctagaaa ctccctgtcaa 1050  
 ggcagcgaga gctgatgcac tcggacagag ctagacactc attcagaagc 1100  
 ttttcgtttt ggccaaagtt gaccactact cttcttactc taacaagcca 1150  
 catgaataga agaattttcc tcaagatgga cccggtaaata ataaccacaa 1200  
 ggaagcgaaa ctgggtgcgt tcaactgagtt ggggttcctaa tctgtttctg 1250  
 gcctgattcc cgcattgagta ttaggggtgat cttaaagagt ttgctcacgt 1300  
 aaacgcccgt gctggggcct gtgaagccag catgttcacc actggtcggt 1350  
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 tgatcgggtg tgcagtgtcc attgtggaga agcttttttg atcagcattt 1550  
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 cataaatgt taaataacct atttttttaa aaaagttaa cttaaggtag 1850  
 aagttccaag ctactagtgt taaattggaa aatatcaata attaagagta 1900  
 ttttaccaca ggaatcctct catggaagtt tactgtgatg ttccttttct 1950  
 cacacaagtt ttagcctttt tcacaaggga actcatactg tctacacatc 2000  
 agaccatagt tgcttaggaa acctttaaaa attccagtta agcaatgttg 2050  
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tgcgaaatca agtctgtcaa gtacaataac atttttaaaa gaaaatggat 2550  
 cccactgttc ctctttgccca cagagaaagc acccagacgc cacaggctct 2600  
 gtcgcatttc aaaacaaacc atgatggagt ggcggccagt ccagcctttt 2650  
 aaagaacgtc aggtggagca gccaggtgaa aggcctggcg gggaggaaaag 2700  
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 aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450  
 gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500  
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 ccca 3554

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 <211> 310  
 <212> PRT  
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 Pro Asp Phe Phe Leu Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly  
 20 25 30  
 Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu  
 35 40 45  
 Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr  
 50 55 60

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr	
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Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly	
				80					85					90	
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val	
				95					100					105	
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	
				110					115					120	
Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val	
				125					130					135	
Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val	
				140					145					150	
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly	
				155					160					165	
His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu	
				170					175					180	
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe	
				185					190					195	
His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala	Val	His	
				200					205					210	
Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp	Ala	
				215					220					225	
Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu	
				230					235					240	
Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val	
				245					250					255	
Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly	
				260					265					270	
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro	
				275					280					285	
Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly	
				290					295					300	
Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile						
				305					310						